

LIB3150-047-Q1-N1-F4 Seq. ID Method BLASTX g3122386 NCBI GI BLAST score 254 4.0e-22 E value Match length 62 79 % identity WD-40 REPEAT PROTEIN MSI1 >gi 2394227 (AF016845) WD-40 NCBI Description repeat protein [Lycopersicon esculentum] 297816 Seq. No. Seq. ID LIB3150-047-Q1-N1-H7 Method BLASTX g4586111 NCBI GI 194 BLAST score 8.0e-15 E value Match length 82 % identity 57 NCBI Description (AL049638) putative protein [Arabidopsis thaliana] Seq. No. Seq. ID LIB3150-048-Q1-N1-B10 Method BLASTX NCBI GI g2245136 BLAST score 154 E value 9.0e-11 64 Match length % identity 44 (Z97344) trehalose-6-phosphate synthase homolog NCBI Description [Arabidopsis thaliana] 297818 Seq. No. LIB3150-048-Q1-N1-C7 Seq. ID Method BLASTX NCBI GI q1184776 BLAST score 271 3.0e-24 E value Match length 67 % identity 82 NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays] 297819 Seq. No. LIB3150-048-Q1-N1-C9 Seq. ID Method BLASTX NCBI GI g1184774 BLAST score 248 E value 6.0e-32 Match length 78 % identity 95 (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC3 [Zea mays]

Seq. No.

Seq. ID LIB3150-048-Q1-N1-D1

297820

Method BLASTN NCBI GI g168606



```
53
BLAST score
                  3.0e-21
E value
                  104
Match length
                  88
% identity
                  Zea mays mitochondrial Rieske Fe-S protein mRNA, complete
NCBI Description
                  297821
Seq. No.
                  LIB3150-048-Q1-N1-F2
Seq. ID
Method
                  BLASTX
                  g4104060
NCBI GI
BLAST score
                  316
                  3.0e-29
E value
                  112
Match length
                   55
% identity
                  (AF031231) S222 [Triticum aestivum]
NCBI Description
                   297822
Seq. No.
                  LIB3150-048-Q1-N1-H10
Seq. ID
                   BLASTN
Method
                   g168419
NCBI GI
                   64
BLAST score
E value
                   1.0e-27
Match length
                   108
% identity
NCBI Description Maize (Z.mays) aldolase mRNA, complete cds
                   297823
Seq. No.
                   LIB3150-048-Q1-N1-H5
Seq. ID
Method
                   BLASTX
                   g1076800
NCBI GI
                   317
BLAST score
                   3.0e-29
E value
                   68
Match length
                   90
% identity
                   L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                   maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
                   peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
                   peroxidase [Zea mays]
                   297824
 Seq. No.
                   LIB3150-049-Q1-N1-A3
 Seq. ID
                   BLASTX
Method
                   g2944417
NCBI GI
                   318
 BLAST score
                   2.0e-29
E value
                   98
Match length
                   64
 % identity
                   (AF049881) peroxidase FLXPER4 [Linum usitatissimum]
 NCBI Description
                   297825
 Seq. No.
                   LIB3150-049-Q1-N1-A5
 Seq. ID
                   BLASTX
 Method
                   g1184776
 NCBI GI
                   377
 BLAST score
```

3.0e-36

107

E value

Match length

NCBI GI

E value

BLAST score

Match length



```
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
                  297826
Seq. No.
                  LIB3150-049-Q1-N1-C7
Seq. ID
                  BLASTX
Method
                  q2286151
NCBI GI
BLAST score
                  326
                  2.0e-30
E value
                  111
Match length
% identity
NCBI Description (AF007580) translation initiation factor [Zea mays]
Seq. No.
                  LIB3150-049-Q1-N1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1345587
                   324
BLAST score
                   4.0e-32
E value
                   97
Match length
                   79
% identity
                   14-3-3-LIKE PROTEIN GF14-6 >gi_998430 bbs 164522 (S77133)
NCBI Description
                   GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                   aa] [Zea mays]
                   297828
Seq. No.
                   LIB3150-049-Q1-N1-D4
Seq. ID
Method
                   BLASTX
                   g118104
NCBI GI
                   479
BLAST score
                   3.0e-48
E value
                   123
Match length
% identity
                   76
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi_82914\overline{8}_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   297829
Seq. No.
                   LIB3150-049-Q1-N1-E1
Seq. ID
                   BLASTX
Method
                   g2464864
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   96
Match length
                   47
 % identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                   297830
 Seq. No.
                   LIB3150-049-Q1-N1-E12
 Seq. ID
                   BLASTX
 Method
```

41794

g4539006

7.0e-42

424



```
% identity
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
                  297831
Seq. No.
                  LIB3150-049-Q1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135411
                  514
BLAST score
                  2.0e-52
E value
                  109
Match length
% identity
                  90
                  TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2
NCBI Description
                  chain - maize >gi_22148_emb_CAA33733_ (X15704)
                  alpha2-tubulin [Zea mays]
                  297832
Seq. No.
Seq. ID
                  LIB3150-049-Q1-N1-F11
Method
                  BLASTX
                  g4193320
NCBI GI
                  405
BLAST score
                  1.0e-39
E value
                  119
Match length
% identity
                  67
NCBI Description (AF045473) histone deacetylase [Zea mays]
                  297833
Seq. No.
                  LIB3150-049-Q1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q134598
                   471
BLAST score
                   2.0e-47
E value
Match length
                   98
                   100
% identity
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                   297834
Seq. No.
                  LIB3150-049-Q1-N1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4039155
                   162
BLAST score
                   4.0e-11
E value
                   110
Match length
                   44
% identity
                   (AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                   [Festuca rubra]
                   297835
Seq. No.
                   LIB3150-049-Q1-N1-G5
Seq. ID
                   BLASTX
Method
                   g112994
NCBI GI
                   262
BLAST score
                   8.0e-23
E value
                   82
Match length
                   71
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
```

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)



ABA-inducible gene protein [Zea mays] >gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 297836

Seq. ID LIB3150-050-Q1-N1-B9

Method BLASTX
NCBI GI g3242789
BLAST score 472
E value 2.0e-47
Match length 130
% identity 62

NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis

thaliana]

Seq. No. 297837

Seq. ID LIB3150-050-Q1-N1-C11

Method BLASTX
NCBI GI g1709619
BLAST score 259
E value 1.0e-22
Match length 99
% identity 56

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /

DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE

(GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)

>gi_2146814_pir__S69181 protein disulfide isomerase (EC
5.3.4.1) precursor - maize >gi_625148 (L39014) protein

disulfide isomerase [Zea mays]

Seq. No. 297838

Seq. ID LIB3150-050-Q1-N1-D11

Method BLASTX
NCBI GI g1321661
BLAST score 265
E value 2.0e-23
Match length 60
% identity 85

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297839

Seq. ID LIB3150-050-Q1-N1-D8

Method BLASTX
NCBI GI g1350986
BLAST score 202
E value 5.0e-16
Match length 69
% identity 64

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No. 297840

Seq. ID LIB3150-050-Q1-N1-D9

Method BLASTX NCBI GI g629861 BLAST score 209 E value 3.0e-21



```
Match length
                  80
% identity
                  zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                  zein Zdl (19 kDa zein) [Zea mays]
                  297841
Seq. No.
                  LIB3150-050-Q1-N1-E6
Seq. ID
                  BLASTX
Method
                   q4585900
NCBI GI
                   228
BLAST score
                   7.0e-19
E value
                   76
Match length
% identity
                   (AC007133) putative histone H2A [Arabidopsis thaliana]
NCBI Description
                   297842
Seq. No.
                   LIB3150-050-Q1-N1-F1
Seq. ID
Method
                   BLASTN
                   g3015620
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   63
Match length
% identity
                   90
                   Zea mays low molecular weight heat shock protein precursor
NCBI Description
                   (hsp22) mRNA, nuclear gene encoding mitochondrial protein,
                   complete cds
                   297843
Seq. No.
                   LIB3150-050-Q1-N1-F7
Seq. ID
Method
                   BLASTX
                   g4455283
NCBI GI
                   178
BLAST score
E value
                   1.0e-17
                   97
Match length
                   55
% identity
                   (AL035527) L1 specific homeobox gene ATML1/ovule-specific
NCBI Description
                   homeobox protein A20 [Arabidopsis thaliana]
                   297844
 Seq. No.
                   LIB3150-050-Q1-N1-G10
 Seq. ID
                   BLASTX
Method
                   g1658313
 NCBI GI
                   206
 BLAST score
                   2.0e-23
 E value
                   85
 Match length
                   34
 % identity
 NCBI Description (Y08987) osr40g2 [Oryza sativa]
                   297845
 Seq. No.
                   LIB3150-050-Q1-N1-G11
 Seq. ID
                   BLASTN
 Method
                   g260552
 NCBI GI
 BLAST score
                    34
                   1.0e-09
 E value
                    38
 Match length
                    97
 % identity
 NCBI Description Wx (wx-B2) {transposable element Tourist-Zm1} [Zea
```

NCBI GI

BLAST score



mays=corn, Transposon Mutant, 150 nt]

```
Seq. No.
                  297846
Seq. ID
                  LIB3150-050-Q1-N1-H11
Method
                  BLASTX
NCBI GI
                  q1885348
BLAST score
                  159
E value
                  3.0e-11
Match length
                  47
% identity
                  77
                  (X91515) histone H4 [Trichogramma caceociae]
NCBI Description
                  297847
Seq. No.
                  LIB3150-050-Q1-N1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1346251
BLAST score
                  208
                  2.0e-16
E value
Match length
                  53
                  79
% identity
NCBI Description
                  HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone
                  [Zea mays]
Seq. No.
                  297848
                  LIB3150-051-Q1-N1-B9
Seq. ID
Method
                  BLASTX
                  q1709000
NCBI GI
                  422
BLAST score
E value
                  1.0e-41
Match length
                  88
% identity
                  92
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 960357 dbj BAA09895 (D63835) S-adenosylmethionine
                  synthetase [Hordeum vulgare]
                  297849
Seq. No.
Seq. ID
                  LIB3150-051-Q1-N1-C10
Method
                  BLASTX
NCBI GI
                  q133961
BLAST score
                  260
                  1.0e-22
E value
Match length
                  68
% identity
                  78
                  40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPRESSOR PROTEIN
NCBI Description
                  SUP44) (RP12) (S2E) >gi 70888 pir R3BYS2 ribosomal protein
                  S2.e - yeast (Saccharomyces cerevisiae) >gi 172793 (M59375)
                  ribosomal protein S4 [Saccharomyces cerevisiae]
                  >gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w
                   [Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_
                   (X94106) SUP44 [Saccharomyces cerevisiae]
Seq. No.
                  297850
Seq. ID
                  LIB3150-051-Q1-N1-C7
Method
                  BLASTX
```

41798

g3334756



2.0e-18 E value 88 Match length 57 % identity

(Y16672) putative arginine/serine-rich splicing factor NCBI Description

[Medicago sativa]

297851 Seq. No.

LIB3150-051-Q1-N1-D5 Seq. ID

BLASTX Method q730536 NCBI GI 529 BLAST score E value 2.0e-54 Match length 103 97

% identity NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal

protein subunit L17 [Nicotiana tabacum]

Seq. No. 297852

LIB3150-051-Q1-N1-G3 Seq. ID

BLASTX Method g1184776 NCBI GI 598 BLAST score E value 3.0e-62Match length 114 100 % identity

(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description

GAPC4 [Zea mays]

297853 Seq. No.

LIB3150-051-Q1-N1-H6 Seq. ID

BLASTX Method g2293566 NCBI GI BLAST score 185 2.0e-16 E value 53 Match length 96 % identity

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

297854 Seq. No.

LIB3150-052-Q1-N1-B2 Seq. ID

BLASTX Method g122087 NCBI GI 471 BLAST score 3.0e-47 E value 120 Match length 81 % identity

HISTONE H3 >gi 81849 pir S04520 histone H3 (clone pH3c-1) NCBI Description

- alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] $> \overline{gi}_4 \overline{8}8565$ (U0 $\overline{9}459$)

histone H3.1 [Medicago sativa] >gi_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

297855 Seq. No.

LIB3150-052-Q1-N1-B5 Seq. ID

```
Method
                  BLASTX
                  g1184774
NCBI GI
BLAST score
                  594
E value
                  1.0e-61
Match length
                  114
                  99
% identity
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
                  297856
Seq. No.
                  LIB3150-052-Q1-N1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22144
BLAST score
                  171
                  1.0e-91
E value
Match length
                  218
                  96
% identity
NCBI Description
                  Maize anaerobically regulated gene for fructose
                  bisphosphate aldolase (EC 4.1.2.13)
Seq. No.
                  297857
Seq. ID
                  LIB3150-052-Q1-N1-E12
Method
                  BLASTX
NCBI GI
                  q131772
BLAST score
                  378
                  2.0e-36
E value
Match length
                  109
% identity
                  74
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  297858
Seq. No.
Seq. ID
                  LIB3150-052-Q1-N1-G11
Method
                  BLASTX
NCBI GI
                  q122022
BLAST score
                  157
                  1.0e-10
E value
Match length
                  60
                  60
% identity
NCBI Description
                  HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat
                  >gi_21801_emb CAA42530 (X59873) histone H2B [Triticum
                  aestivum]
Seq. No.
                  297859
Seq. ID
                  LIB3150-052-Q1-N1-G3
```

Method BLASTX
NCBI GI g133867
BLAST score 493
E value 6.0e-50
Match length 120
% identity 78

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal

protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 297860



```
LIB3150-053-Q1-N1-A6
Seq. ID
Method
                  BLASTX
                  q70644
NCBI GI
                  592
BLAST score
                  1.0e-61
E value
                  125
Match length
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
                  297861
Seq. No.
                  LIB3150-053-Q1-N1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914402
                  247
BLAST score
                  3.0e-21
E value
                  97
Match length
                  57
% identity
                  PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO I)
NCBI Description
                   (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME I) (PPX I)
                  >gi 2370333_emb_CAA73865_ (Y13465) protoporphyrinogen
                  oxidase [Nicotiana tabacum]
Seq. No.
                   297862
                  LIB3150-053-Q1-N1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120670
                   495
BLAST score
                   3.0e-50
E value
                   121
Match length
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) C - maize
                   >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.
                   297863
                   LIB3150-053-Q1-N1-D8
Seq. ID
                   BLASTX
Method
                   g266398
NCBI GI
BLAST score
                   169
                   3.0e-12
E value
                   62
Match length
                   55
 % identity
                   TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                   INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
                   inhibitor precursor - maize >gi 22327 emb CAA37998
                   (X54064) corn Hageman factor inhibitor [Zea mays]
                   297864
 Seq. No.
                   LIB3150-053-Q1-N1-E12
 Seq. ID
                   BLASTX
 Method
                   q2864625
 NCBI GI
                   522
 BLAST score
                   2.0e-53
 E value
                   112
 Match length
                   86
 % identity
 NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
```

```
297865
Seq. No.
                  LIB3150-053-Q1-N1-E9
Seq. ID
Method
                  BLASTX
                  g70644
NCBI GI
                  291
BLAST score
                  1.0e-26
E value
                  94
Match length
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
                  297866
Seq. No.
                  LIB3150-054-Q1-N1-A10
Seq. ID
                  BLASTX
Method
                   q4506491
NCBI GI
                   281
BLAST score
                   4.0e-25
E value
Match length
                   89
% identity
                   replication factor C (activator 1) 4 (37kD)
NCBI Description
                   >gi 1703052 sp P35249_AC12_HUMAN ACTIVATOR 1 37 KD SUBUNIT
                   (REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT)
                   (RF-C 37 KD SUBUNIT) (RFC37) >gi_1498256 (M87339)
                   replication factor C, 37-kDa subunit [Homo sapiens]
                   297867
Seq. No.
                   LIB3150-054-Q1-N1-B2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3821780
                   36
BLAST score
                   9.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   297868
Seq. No.
                   LIB3150-054-Q1-N1-D7
Seq. ID
Method
                   BLASTX
                   q1654140
NCBI GI
                   340
BLAST score
                   5.0e-32
E value
                   101
Match length
                   57
 % identity
                   (U37840) lipoxygenase [Lycopersicon esculentum]
NCBI Description
                   297869
 Seq. No.
                   LIB3150-054-Q1-N1-D8
 Seq. ID
                   BLASTX
 Method
                   g3548802
 NCBI GI
                   149
 BLAST score
                   4.0e-10
 E value
                   41
 Match length
                   66
 % identity
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
 NCBI Description
```

[Nicotiana tabacum] [Arabidopsis thaliana]

>gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein



```
297870
Seq. No.
                  LIB3150-054-Q1-N1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399854
BLAST score
                  241
                  2.0e-20
E value
Match length
                  71
                  73
% identity
NCBI Description HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
                  >gi 22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]
Seq. No.
                  297871
                  LIB3150-054-Q1-N1-G5
Seq. ID
Method
                  BLASTX
                  g2492504
NCBI GI
                  156
BLAST score
                  1.0e-10
E value
Match length
                  108
                   41
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                  >gi 1669660 emb CAA70565_ (Y09396) protein of AAA family
                   [Capsicum annuum]
Seq. No.
                   297872
                  LIB3150-054-Q1-N1-G6
Seq. ID
                  BLASTX
Method
                  q3608145
NCBI GI
                   186
BLAST score
E value
                   6.0e-14
Match length
                   62
                   63
% identity
                  (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   297873
Seq. No.
                   LIB3150-054-Q1-N1-H10
Seq. ID
                   BLASTX
Method
                   g4519539
NCBI GI
                   182
BLAST score
                   1.0e-13
E value
                   64
Match length
                   56
% identity
                   (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                   domestica]
                   297874
Seq. No.
                   LIB3150-055-Q1-N1-A9
Seq. ID
                   BLASTX
Method
                   g2266666
NCBI GI
                   380
BLAST score
                   1.0e-36
E value
                   82
Match length
                   83
% identity
                  (Y14202) hypothetical protein [Hordeum vulgare]
NCBI Description
                   297875
Seq. No.
Seq. ID
                   LIB3150-055-Q1-N1-D10
```

BLASTN

Method

```
g1256711
NCBI GI
                  74
BLAST score
                  1.0e-33
E value
                  224
Match length
                  82
% identity
NCBI Description Zea mays O-methyltransferase (OMT) gene, complete cds
                  297876
Seq. No.
                  LIB3150-056-Q1-N1-A3
Seq. ID
Method
                  BLASTN
                  g340933
NCBI GI
                  60
BLAST score
                  3.0e-25
E value
                  72
Match length
                  96
% identity
NCBI Description Zea mays 10-kDa zein gene, complete cds
                  297877
Seq. No.
                  LIB3150-056-Q1-N1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1666173
BLAST score
                  430
E value
                  1.0e-42
                  92
Match length
                  90
% identity
NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]
                  297878
Seq. No.
                  LIB3150-056-Q1-N1-D3
Seq. ID
                  BLASTX
Method
                  g119355
NCBI GI
                   495
BLAST score
E value
                   3.0e-50
                   99
Match length
                   99
% identity
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
                   297879
Seq. No.
                   LIB3150-056-Q1-N1-D9
Seq. ID
                   BLASTX
Method
                   q464705
NCBI GI
                   162
BLAST score
                   3.0e-11
E value
                   32
Match length
                   94
% identity
                   40S RIBOSOMAL PROTEIN S13 >gi_419802_pir__S30146 ribosomal
NCBI Description
                   protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455)
                   cytoplasmatic ribosomal protein S13 [Zea mays]
                   297880
Seq. No.
Seq. ID
                   LIB3150-057-Q1-N1-A6
                   BLASTX
Method
```

q1632831

NCBI GI

NCBI GI BLAST score

E value

Match length

301 5.0e-28

59

```
171
BLAST score
                  1.0e-12
E value
                  36
Match length
                  89
% identity
                 (Z49698) orf [Ricinus communis]
NCBI Description
                  297881
Seq. No.
                  LIB3150-057-Q1-N1-B5
Seq. ID
                  BLASTX
Method
                  g2642648
NCBI GI
                  289
BLAST score
                  4.0e-26
E value
                  67
Match length
                  88
% identity
                   (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                   [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                   shock 70 protein [Spinacia oleracea] >gi 2660770 (AF034617)
                   cytosolic heat shock 70 protein [Spinacia oleracea]
                   297882
Seq. No.
                  LIB3150-057-Q1-N1-B6
Seq. ID
Method
                  BLASTX
                   g4580990
NCBI GI
                   170
BLAST score
                   2.0e-14
E value
                   96
Match length
                   48
% identity
                   (AF120335) putative transposase [Arabidopsis thaliana]
NCBI Description
                   297883
Seq. No.
                   LIB3150-057-Q1-N1-B9
Seq. ID
                   BLASTX
Method
                   g2911067
NCBI GI
                   160
BLAST score
                   3.0e-11
E value
                   80
Match length
% identity
                   (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis
NCBI Description
                   thaliana]
                   297884
Seq. No.
                   LIB3150-057-Q1-N1-G10
Seq. ID
                   BLASTX
Method
                   q4056502
NCBI GI
                   170
BLAST score
                   3.0e-12
E value
                   53
Match length
                   62
 % identity
                   (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                   297885
 Seq. No.
Seq. ID
                   LIB3150-057-Q1-N1-H9
                   BLASTX
Method
                   q2340947
```



% identity (X98497) ESR1g1 [Zea mays] >gi 2340951_emb_CAA68230_ NCBI Description (X99968) ESR1g2 [Zea mays] 297886 Seq. No. LIB3150-058-Q1-N1-A3 Seq. ID BLASTX Method g100857 NCBI GI 571 BLAST score 5.0e-59 E value 115 Match length 97 % identity NCBI Description Bronze-2 protein - Maize 297887 Seq. No. LIB3150-058-Q1-N1-B1 Seq. ID BLASTX Method g118104 NCBI GI 371 BLAST score 1.0e-35 E value 95 Match length 76 % identity PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) NCBI Description (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) - $\overline{\text{maize}} > \overline{\text{gi}} 168\overline{46}1 \text{ (M55021)} \text{ cyclophilin [Zea mays]}$ >gi $82914\overline{8}$ _emb_CAA48638_ (X68678) cyclophilin [Zea mays] 297888 Seq. No. LIB3150-058-Q1-N1-B11 Seq. ID BLASTX Method g1620753 NCBI GI 156 BLAST score 2.0e-10 E value 63 Match length 48 % identity (U72942) proteinase inhibitor [Oryza sativa] NCBI Description >gi 2829212 gb AAC00503 (AF044059) proteinase inhibitor [Oryza sativa] 297889 Seq. No. LIB3150-058-Q1-N1-C10 Seq. ID BLASTX Method g3790100 NCBI GI 213 BLAST score 3.0e-17 E value 112 Match length 49 % identity (AF095520) pyrophosphate-dependent phosphofructokinase beta NCBI Description subunit [Citrus X paradisi] 297890 Seq. No.

Seq. ID LIB3150-058-Q1-N1-E11

Method BLASTX
NCBI GI g1184776
BLAST score 176
E value 5.0e-20



```
91
Match length
                   65
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   297891
Seq. No.
                   LIB3150-058-Q1-N1-F3
Seq. ID
                   BLASTN
Method
                   q3851527
NCBI GI
                   54
BLAST score
                   2.0e-21
E value
Match length
                   141
% identity
                   85
                   Hordeum vulgare cultivar Bomi starch branching enzyme IIb
NCBI Description
                   (sbeIIb) gene, nuclear gene encoding plastid protein,
                   partial cds
                   297892
Seq. No.
                   LIB3150-058-Q1-N1-G6
Seq. ID
                   BLASTX
Method
                   g2282584
NCBI GI
                   457
BLAST score
                   7.0e-46
E value
Match length
                   103
% identity
                   (U76259) elongation factor 1-alpha [Zea mays]
NCBI Description
                   297893
Seq. No.
                   LIB3150-059-Q1-N1-A8
Seq. ID
Method
                   BLASTX
                   g82705
NCBI GI
                   264
BLAST score
                   3.0e-23
E value
                   74
Match length
 % identity
                   lipid body-associated major protein L3 - maize (fragment)
NCBI Description
                   >gi_168513 (M17225) major protein L3 [Zea mays]
                   297894
 Seq. No.
                   LIB3150-059-Q1-N1-B10
 Seq. ID
                   BLASTX
 Method
                    g118104
 NCBI GI
 BLAST score
                    341
                    4.0e-34
 E value
                    97
 Match length
                    77
 % identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
 NCBI Description
                    (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                    >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                    maize > gi_168\overline{46}1 (M55021) cyclophilin [Zea mays]
                    >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                    297895
 Seq. No.
                    LIB3150-059-Q1-N1-C10
 Seq. ID
                    BLASTX
 Method
```

q1184776

569

NCBI GI

BLAST score



```
E value
                  7.0e-59
Match length
                  108
% identity
                  100
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
                  297896
Seq. ID
                  LIB3150-059-Q1-N1-C11
Method
                  BLASTX
NCBI GI
                  q133867
BLAST score
                  258
E value
                  1.0e-22
Match length
                  83
% identity
                  64
                  40S RIBOSOMAL PROTEIN S11 >qi 82722 pir S16577 ribosomal
NCBI Description
                  protein S11 - maize >qi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
                  297897
Seq. No.
Seq. ID
                  LIB3150-059-Q1-N1-C8
Method
                  BLASTX
NCBI GI
                  g134613
BLAST score
                  321
                  9.0e-30
E value
                  74
Match length
                  84
% identity
                  SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi 82727 pir A29077
NCBI Description
                  superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize
                  >gi 168620 (M54936) superoxide dismutase 2 [Zea mays]
                  >gi 168622 (M15175) SOD2 protein [Zea mays]
Seq. No.
                  297898
Seq. ID
                  LIB3150-059-Q1-N1-D10
Method
                  BLASTX
NCBI GI
                  q129916
BLAST score
                  238
                  3.0e-20
E value
Match length
                  60
% identity
                  80
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                  (AA 1 - 401) [Triticum aestivum]
Seq. No.
                  297899
Seq. ID
                  LIB3150-059-Q1-N1-D11
Method
                  BLASTX
NCBI GI
                  q3334138
BLAST score
                  269
E value
                  5.0e-28
Match length
                  94
% identity
                  66
NCBI Description
                  CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
                  [Glycine max]
```

Seq. No. 297900

Seq. ID LIB3150-059-Q1-N1-D12



```
BLASTX
Method
                  g3983663
NCBI GI
                   554
BLAST score
                   4.0e-57
E value
                  124
Match length
                   85
% identity
NCBI Description (AB011270) importin-betal [Oryza sativa]
                   297901
Seq. No.
                  LIB3150-059-Q1-N1-D6
Seq. ID
                   BLASTN
Method
                   g899607
NCBI GI
                   50
BLAST score
                   1.0e-19
E value
                   94
Match length
                   58
% identity
NCBI Description Zea mays polyubiquitin (MubC5) mRNA, complete cds
                   297902
Seq. No.
                   LIB3150-060-Q1-N1-C2
Seq. ID
                   BLASTX
Method
                   g4056483
NCBI GI
                   146
BLAST score
                   1.0e-09
E value
                   71
Match length
                   48
% identity
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]
                   297903
Seq. No.
                   LIB3150-060-Q1-N1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2914700
                   261
BLAST score
                   3.0e-23
E value
                   58
Match length
                   84
% identity
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thaliana]
                   297904
Seq. No.
Seq. ID
                   LIB3150-060-Q1-N1-D10
                   BLASTX
Method
NCBI GI
                   q1184776
                   177
BLAST score
                   1.0e-17
E value
                   61
Match length
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   297905
Seq. No.
                   LIB3150-060-Q1-N1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2642213
BLAST score
                   159
```

2.0e-14

45

E value Match length



% identity (AF030385) nitrate-induced NOI protein [Zea mays] NCBI Description >gi 2895781 (AF045033) nitrate-induced NOI protein [Zea mays] 297906 Seq. No. LIB3150-060-Q1-N1-H10 Seq. ID BLASTX Method q1184776 NCBI GI 151 BLAST score 4.0e-10 E value Match length 58 % identity (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC4 [Zea mays] 297907 Seq. No. LIB3150-061-Q1-N1-D1 Seq. ID BLASTX Method g135398 NCBI GI 272 BLAST score 2.0e-34 E value Match length 94 % identity 76 TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1 NCBI Description chain - maize >gi_22147_emb_CAA33734_ (X15704) alpha1-tubulin [Zea mays] 297908 Seq. No. LIB3150-063-P2-K1-A8 Seq. ID Method BLASTN q1575127 NCBI GI BLAST score 92 2.0e-44 E value 136 Match length 92 % identity Zea mays lumenal binding protein cBiPe2 mRNA, complete cds NCBI Description 297909 Seq. No. LIB3150-063-P2-K1-H6 Seq. ID BLASTN Method g1037129 NCBI GI 59 BLAST score 8.0e-25 E value 83 Match length 93 % identity (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, NCBI Description Tuxpeno CMS 450, mRNA Partial, 1889 nt] 297910 Seq. No. LIB3150-064-P1-N1-A5 Seq. ID

BLASTX Method q1708107 NCBI GI 312 BLAST score 1.0e-28 E value Match length 87 76 % identity



```
NCBI Description HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]
                  297911
Seq. No.
                  LIB3150-064-P1-N1-B8
Seq. ID
                  BLASTX
Method
                  g2828280
NCBI GI
                  400
BLAST score
                  5.0e-39
E value
                  101
Match length
                  72
% identity
                  (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 2832633 emb CAA16762 (AL021711) putative protein
                   [Arabidopsis thaliana]
                   297912
Seq. No.
                  LIB3150-064-P1-N1-H1
Seq. ID
                  BLASTX
Method
                   g113460
NCBI GI
                   291
BLAST score
                   3.0e-26
E value
                   84
Match length
% identity
                   70
                  ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                   >gi_100851_pir__S16568 ADP,ATP carrier protein precursor -
                   maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide
                   translocator [Zea mays]
                   297913
Seq. No.
                   LIB3150-064-P2-K1-B5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q902585
                   38
BLAST score
                   3.0e-12
E value
                   46
Match length
                   96
% identity
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
                   297914
Seq. No.
                   LIB3150-064-P2-K1-B7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2340954
BLAST score
                   193
                   1.0e-104
E value
                   213
Match length
                   98
% identity
NCBI Description Z.mays ESR3g2 gene, clone L42a4
                   297915
Seq. No.
Seq. ID
                   LIB3150-064-P2-K1-D8
                   BLASTX
Method
NCBI GI
                   q4519539
BLAST score
                   153
                   5.0e-14
E value
Match length
                   124
                   39
% identity
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
```



domestica]

```
297916
Seq. No.
                  LIB3150-064-P2-K1-F4
Seq. ID
                  BLASTX
Method
                  g2829869
NCBI GI
                  249
BLAST score
                  3.0e-21
E value
                  69
Match length
                  65
% identity
                   (AC002396) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
                  297917
Seq. No.
                  LIB3150-064-P2-K1-G2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1184775
                   40
BLAST score
                   2.0e-13
E value
                  72
Match length
% identity
                   89
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
NCBI Description
                   (gpc4) mRNA, complete cds
                   297918
Seq. No.
                   LIB3150-064-P2-K1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g606969
                   35
BLAST score
                   2.0e-10
E value
                   71
Match length
                   87
% identity
                  Arabidopsis thaliana cytoplasmic ribosomal protein L18
NCBI Description
                   mRNA, complete cds
                   297919
Seq. No.
Seq. ID
                   LIB3150-065-P2-K1-A3
                   BLASTX
Method
                   g1321661
NCBI GI
                   154
BLAST score
                   3.0e-10
E value
                   39
Match length
                   79
% identity
                   (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                   297920
Seq. No.
Seq. ID
                   LIB3150-065-P2-K1-B10
Method
                   BLASTN
NCBI GI
                   q3851000
BLAST score
                   151
                   2.0e-79
E value
Match length
                   267
% identity
                   Zea mays pyruvate dehydrogenase El beta subunit isoform 2
NCBI Description
                   mRNA, nuclear gene encoding mitochondrial protein, complete
```



```
297921
Seq. No.
                  LIB3150-065-P2-K1-B7
Seq. ID
Method
                  BLASTX
                  q2459446
NCBI GI
                  232
BLAST score
                  1.0e-19
E value
                  90
Match length
                  52
% identity
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                  thaliana]
                   297922
Seq. No.
                  LIB3150-065-P2-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1350983
                   211
BLAST score
                   1.0e-16
E value
                   86
Match length
                   51
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                   297923
Seq. No.
                   LIB3150-065-P2-K1-C6
Seq. ID
Method
                   BLASTN
                   g168584
NCBI GI
                   80
BLAST score
                   5.0e-37
E value
                   215
Match length
                   92
% identity
NCBI Description Corn pyruvate, orthophosphate dikinase gene, exons 2-19
                   297924
Seq. No.
                   LIB3150-065-P2-K1-D5
Seq. ID
Method
                   BLASTX
                   q2129553
NCBI GI
BLAST score
                   319
E value
                   2.0e-29
                   79
Match length
                   72
% identity
NCBI Description calcium-dependent protein kinase 6 - Arabidopsis thaliana
                   297925
 Seq. No.
                   LIB3150-065-P2-K1-F4
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g168419
 BLAST score
                   82
E value
                   2.0e-38
Match length
                   155
 % identity
                   89
 NCBI Description Maize (Z.mays) aldolase mRNA, complete cds
                   297926
 Seq. No.
                   LIB3150-065-P2-K1-G3
 Seq. ID
                   BLASTN
 Method
                   g1917018
 NCBI GI
                   80
 BLAST score
```

6.0e-37

E value



```
Match length
% identity
                  90
                  Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA,
NCBI Description
                  complete cds
                  297927
Seq. No.
                  LIB3150-065-P2-K1-G8
Seq. ID
                  BLASTN
Method
                  g22312
NCBI GI
                  52
BLAST score
                  2.0e-20
E value
                  180
Match length
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
                   297928
Seq. No.
                  LIB3150-066-P1-N1-A10
Seq. ID
                  BLASTX
Method
                   q2181180
NCBI GI
                   144
BLAST score
                   3.0e-09
E value
                   80
Match length
% identity
                  (Z84377) xylosidase [Aspergillus niger]
NCBI Description
                   297929
Seq. No.
Seq. ID
                   LIB3150-066-P1-N1-B3
Method
                   BLASTX
                   g1184774
NCBI GI
                   326
BLAST score
                   1.0e-30
E value
                   69
Match length
% identity
                   91
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   297930
Seq. No.
                   LIB3150-066-P1-N1-F1
Seq. ID
                   BLASTN
Method
                   g1276936
NCBI GI
                   52
BLAST score
                   1.0e-20
E value
                   76
Match length
                   92
 % identity
                  Zea mays USDA Ames 8212 ITS1, 5.8S ribosomal RNA, ITS2
NCBI Description
                   297931
 Seq. No.
                   LIB3150-066-P1-N1-G4
 Seq. ID
                   BLASTX
Method
                   g1658315
NCBI GI
```

(Y08988) osr40g3 [Oryza sativa]

347

99

69

7.0e-33

BLAST score

Match length

NCBI Description

% identity

E value



```
297932
Seq. No.
                  LIB3150-066-P2-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1498064
                  251
BLAST score
                  2.0e-21
E value
Match length
                  81
                  63
% identity
                  (U64825) AtE1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  297933
Seq. ID
                  LIB3150-066-P2-K1-G10
Method
                  BLASTN
                  g2282583
NCBI GI
                  84
BLAST score
                  2.0e-39
E value
                  152
Match length
% identity
                  89
                  Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete
NCBI Description
                  297934
Seq. No.
Seq. ID
                  LIB3150-066-P2-K1-G4
Method
                  BLASTN
                  g296203
NCBI GI
                  43
BLAST score
                  6.0e-15
E value
                  79
Match length
% identity
                  89
NCBI Description P. miliaceum mRNA for alanine aminotransferase
                  297935
Seq. No.
                  LIB3150-066-P2-K1-H2
Seq. ID
                  BLASTX
Method
                  g464707
NCBI GI
                   283
BLAST score
                   3.0e-25
E value
                  70
Match length
                   77
% identity
                  40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                   >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi_434343 emb CAA82273 (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >qi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                   [Arabidopsis thaliana] >gi 434906 emb CAA82275_ (Z28962)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >qi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                   ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                   thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                   gb R30430 come from this gene. [Arabidopsis thaliana]
                   >qi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                   protein [Arabidopsis thaliana]
```

Seq. No. 297936

Seq. ID LIB3150-067-P1-N1-E2

NCBI GI



```
BLASTX
Method
                   g82512
NCBI GI
                   171
BLAST score
                   2.0e-12
E value
                   37
Match length
                   47
 % identity
                   ubiquitin precursor - rice (fragment)
 NCBI Description
                   >gi 218189 dbj BAA02241_ (D12776) poly-ubiquitin [Oryza
                   sativa]
                   297937
 Seq. No.
 Seq. ID
                   LIB3150-067-P1-N1-G4
                   BLASTN
 Method
                   g22176
 NCBI GI
                   163
 BLAST score
                   1.0e-86
 E value
                   289
 Match length
                   89
 % identity
 NCBI Description Z.mays P gene
                   297938
 Seq. No.
                   LIB3150-067-P2-K1-A6
 Seq. ID
                   BLASTX
 Method
                   q2511531
 NCBI GI
                   197
 BLAST score
                   9.0e-16
 E value
Match length
                   49
                   73
 % identity
                    (AF008120) alpha tubulin 1 [Eleusine indica]
 NCBI Description
                   >gi 3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                    [Eleusine indica]
                   297939
 Seq. No.
                   LIB3150-067-P2-K1-B12
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   q2286150
                    151
 BLAST score
                    3.0e-79
 E value
                    331
 Match length
                    85
 % identity
                   Zea mays translation initiation factor (eIF-4A) mRNA,
 NCBI Description
                    complete cds
                    297940
 Seq. No.
                    LIB3150-067-P2-K1-D4
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    q168482
 BLAST score
                    95
                    3.0e-46
 E value
 Match length
                    159
                    91
 % identity
                   Corn starch branching enzyme II mRNA, complete cds
 NCBI Description
 Seq. No.
                    297941
                    LIB3150-067-P2-K1-D6
 Seq. ID
                    BLASTN
 Method
```

41816

g2668741

NCBI GI

E value

BLAST score

Match length

q1709619

5.0e-25

280

57



```
BLAST score
                  7.0e-88
E value
                  248
Match length
                  92
% identity
                  Zea mays glycine-rich RNA binding protein (GRP) mRNA,
NCBI Description
                  complete cds
                  297942
Seq. No.
                  LIB3150-067-P2-K1-F3
Seq. ID
                  BLASTX
Method
                  g1172836
NCBI GI
                  169
BLAST score
                  3.0e-12
E value
                  46
Match length
                  76
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
NCBI Description
                  small ras-related protein [Nicotiana tabacum]
                  297943
Seq. No.
Seq. ID
                  LIB3150-067-P2-K1-G2
                  BLASTX
Method
NCBI GI
                  g4096786
BLAST score
                  168
                  7.0e-12
E value
                  35
Match length
                  94
% identity
                  (U39958) NADP-malic enzyme [Zea mays]
NCBI Description
                  297944
Seq. No.
Seq. ID
                  LIB3150-068-P1-N1-B6
                  BLASTX
Method
NCBI GI
                   g4467099
BLAST score
                   221
                   4.0e-18
E value
                   72
Match length
                   71
% identity
                   (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   297945
Seq. No.
Seq. ID
                   LIB3150-068-P1-N1-C2
Method
                   BLASTX
NCBI GI
                   g1184774
                   271
BLAST score
                   5.0e-24
E value
Match length
                   74
% identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   297946
Seq. No.
Seq. ID
                   LIB3150-068-P1-N1-C5
                   BLASTX
Method
```

Seq. ID

Method NCBI GI



```
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
NCBI Description
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                  (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi_625148 (L39014) protein
                  disulfide isomerase [Zea mays]
                  297947
Seq. No.
                  LIB3150-068-P1-N1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1835729
                  159
BLAST score
                  8.0e-11
E value
                  38
Match length
                  87
% identity
                  (U86017) ribosomal protein [Oryza sativa]
NCBI Description
                  297948
Seq. No.
                  LIB3150-068-P1-N1-F8
Seq. ID
                  BLASTX
Method
                  g136632
NCBI GI
BLAST score
                  250
E value
                   5.0e-22
                   61
Match length
                   82
% identity
                  UBIQUITIN-ACTIVATING ENZYME E1 1 >gi_100841_pir__A38373
NCBI Description
                   ubiquitin--protein ligase (EC 6.3.2.\overline{19}) E1 - wheat
                   >gi 285451_pir_ A42873 ubiquitin-activating enzyme E1, UBA1
                   - Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1
                   [Triticum aestivum]
                   297949
Seq. No.
                   LIB3150-068-P1-N1-H6
Seq. ID
Method
                   BLASTN
                   q22101
NCBI GI
BLAST score
                   41
                   6.0e-14
E value
Match length
                   132
                   83
% identity
NCBI Description Maize 7SL RNA of signal recognition particle
Seq. No.
                   297950
                   LIB3150-068-P2-K1-B11
Seq. ID
                   BLASTX
Method
                   q1350777
NCBI GI
                   237
BLAST score
                   7.0e-20
E value
                   71
Match length
                   66
 % identity
                   60S RIBOSOMAL PROTEIN L9 >gi 971282_dbj_BAA07209_ (D38012)
NCBI Description
                   ribosomal protein L9 [Oryza sativa]
                   297951
 Seq. No.
```

41818

LIB3150-068-P2-K1-C7

BLASTN

g22144



```
BLAST score
                  1.0e-135
E value
                  260
Match length
                   98
% identity
                  Maize anaerobically regulated gene for fructose
NCBI Description
                  bisphosphate aldolase (EC 4.1.2.13)
                   297952
Seq. No.
                   LIB3150-068-P2-K1-F12
Seq. ID
Method
                  BLASTX
                   g1350777
NCBI GI
BLAST score
                   234
                   1.0e-19
E value
                   53
Match length
                   85
% identity
                   60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209 (D38012)
NCBI Description
                   ribosomal protein L9 [Oryza sativa]
                   297953
Seq. No.
                   LIB3150-068-P2-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1707017
BLAST score
                   272
                   6.0e-24
E value
                   66
Match length
                   74
% identity
                   (U78721) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
                   297954
Seq. No.
                   LIB3150-068-P2-K1-H3
Seq. ID
                   BLASTX
Method
                   g556401
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
Match length
                   55
% identity
                   51
                  (M28159) glutelin [Oryza sativa]
NCBI Description
                   297955
Seq. No.
                   LIB3150-068-P2-K1-H8
Seq. ID
                   BLASTX
Method
                   q3970823
NCBI GI
                   288
BLAST score
                   9.0e-26
E value
                   56
Match length
                   98
 % identity
                  (X17555) pyruvate decarboxylase [Zea mays]
 NCBI Description
                   297956
 Seq. No.
                   LIB3150-069-P1-N1-B6
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g118104
 BLAST score
                   184
                    3.0e-14
 E value
                    39
 Match length
```

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

92

% identity



(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) maize >gi 168461 (M55021) cyclophilin [Zea mays] >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]

297957 Seq. No.

LIB3150-069-P1-N1-D8 Seq. ID

Method BLASTX g232031 NCBI GI 142 BLAST score 3.0e-09 E value Match length 36 75 % identity

ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224 NCBI Description

translation elongation factor eEF-1 beta chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'

[Oryza sativa]

297958 Seq. No.

LIB3150-069-P1-N1-F1 Seq. ID

Method BLASTX g2244990 NCBI GI BLAST score 187 4.0e-14E value 37 Match length 100 % identity

(Z97340) similarity to LIM homeobox protein -NCBI Description

Caenorhabditis [Arabidopsis thaliana]

297959 Seq. No.

LIB3150-069-P1-N1-F7 Seq. ID

BLASTX Method g1350783 NCBI GI 160 BLAST score 5.0e-11 E value 97 Match length 39 % identity

RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR NCBI Description

>gi 282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana]

>gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein

kinase 5 precursor (RLK5) [Arabidopsis thaliana]

297960 Seq. No.

Seq. ID LIB3150-069-P1-N1-H6

BLASTX Method g1173055 NCBI GI 152 BLAST score 4.0e-22 E value 94 Match length 60 % identity

60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 NCBI Description

ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090

(X78284) RL5 ribosomal protein [Medicago sativa]



```
297961
Seq. No.
                  LIB3150-069-P2-K1-C11
Seq. ID
                  BLASTN
Method
                  g1037129
NCBI GI
                  58
BLAST score
                  4.0e-24
E value
                  86
Match length
                  92
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  297962
Seq. No.
                  LIB3150-069-P2-K1-D8
Seq. ID
                  BLASTN
Method
                  g22272
NCBI GI
                  80
BLAST score
                  4.0e-37
E value
                  167
Match length
                  87
% identity
                  Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
NCBI Description
                  297963
Seq. No.
                  LIB3150-069-P2-K1-F2
Seq. ID
                  BLASTX
Method
                   g567890
NCBI GI
                   153
BLAST score
                   5.0e-10
E value <
                   129
Match length
                   38
% identity
                   (L37352) beta-galactosidase-complementation protein
NCBI Description
                   [Cloning vector]
                   297964
Seq. No.
                   LIB3150-069-P2-K1-F4
Seq. ID
                   BLASTX
Method
                   q135417
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
Match length
                   74
                   66
% identity
                   TUBULIN ALPHA-3 CHAIN >qi 100946 pir JN0105 tubulin
NCBI Description
                   alpha-3 chain - maize >gi 22150 emb CAA44861 (X63176)
                   Alpha-tubulin #3 [Zea mays] >gi_485\overline{3}77 (M60171) alpha-3
                   tubulin [Zea mays]
                   297965
Seq. No.
Seq. ID
                   LIB3150-069-P2-K1-G9
                   BLASTX
Method
                   q464706
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
Match length
                   43
                   77
% identity
                   40S RIBOSOMAL PROTEIN S15 (S12) >gi_1078669_pir__A53793
NCBI Description
                   ribosomal protein S12, cytosolic - Podospora anserina
                   >qi 401841 emb CAA80805 (Z23267) cytoplasmic ribosomal
```

protein S12 [Podospora anserina]



```
297966
Seq. No.
                  LIB3150-070-P1-N1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1084457
BLAST score
                  158
                  7.0e-11
E value
                  51
Match length
% identity
                  elongation factor 1-beta - Rice >gi 432368 dbj BAA04903_
NCBI Description
                   (D23674) elongation factor 1 beta [Oryza sativa]
Seq. No.
Seq. ID
                  LIB3150-070-P1-N1-D10
                  BLASTN
Method
                  g829147
NCBI GI
                  51
BLAST score
                   4.0e-20
E value
Match length
                  139
                   84
% identity
                  Z.mays gene for cyclophilin
NCBI Description
                  297968
Seq. No.
Seq. ID
                  LIB3150-071-P1-N1-C7
                  BLASTX
Method
NCBI GI
                   g82696
                   187
BLAST score
                   2.0e-14
E value
Match length
                   46
                   78
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   297969
Seq. No.
Seq. ID
                   LIB3150-071-P1-N1-D11
Method
                   BLASTX
NCBI GI
                   g399414
BLAST score
                   245
                   7.0e-21
E value
Match length
                   78
% identity
                   65
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_322865_pir_ JC1454 translation elongation factor eEF-1
                   alpha chain - wheat >gi_170776 (M90077) translation
                   elongation factor 1 alpha-subunit [Triticum aestivum]
                   >gi 949878 emb CAA90651 (Z50789) elongation factor 1-alpha
                   [Hordeum vulgare]
                   297970
Seq. No.
                   LIB3150-071-P1-N1-D6
Seq. ID
Method
                   BLASTX
                   q1184776
NCBI GI
                   265
BLAST score
                   2.0e-23
E value
Match length
                   76
```

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

75

% identity



GAPC4 [Zea mays]

```
47.
                   297971
Seq. No.
                   LIB3150-071-P1-N1-E12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22172
BLAST score
                   61
                   6.0e-26
E value
Match length
                   61
                   100
% identity
                   Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit
NCBI Description
                   297972
Seq. No.
                   LIB3150-071-P1-N1-E2
Seq. ID
Method
                   BLASTX
                   g122007
NCBI GI
BLAST score
                   142
                   5.0e-09
E value
                   38
Match length
                   79
% identity
                   HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >gi_20448_emb_C\overline{A}A37828_ (X\overline{53}831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
Seq. No.
                   297973
                   LIB3150-071-P1-N1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4038461
BLAST score
                   187
                   3.0e-14
E value
                   72
Match length
                   51
% identity
                   (AF107772) TcSTI1 [Trypanosoma cruzi]
NCBI Description
                   297974
Seq. No.
                   LIB3150-071-P1-N1-F1
Seq. ID
                   BLASTX
Method
                   g2723473
NCBI GI
                   155
BLAST score
                   2.0e-23
E value
                   94
Match length
                   67
% identity
                   (D89726) defender against apoptotic death 1 protein [Oryza
NCBI Description
                   sativa] >gi_2723883_dbj_BAA24104_ (D89727) defender against
                   apoptotic death 1 protein [Oryza sativa]
                   297975
Seq. No.
                   LIB3150-071-P1-N1-F2
Seq. ID
                   BLASTX
Method
                   g2642158
NCBI GI
BLAST score
                   221
E value
                   5.0e-18
```

% identity

Match length

(AC003000) hypothetical protein [Arabidopsis thaliana] NCBI Description

297976 Seq. No.

83 55

Match length

% identity

87 47



```
LIB3150-071-P1-N1-F7
Seq. ID
                  BLASTX
Method
                  g3122071
NCBI GI
                  419
BLAST score
                  2.0e-42
E value
                  106
Match length
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi 2130148 pir S66339 translation elongation factor eEF-1
                  alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
                  alpha subunit of tlanslation elongation factor 1 [Zea mays]
                  297977
Seq. No.
                  LIB3150-071-P1-N1-F8
Seq. ID
                  BLASTN
Method
                  g4185305
NCBI GI
BLAST score
                   44
                  1.0e-15
E value
                   60
Match length
                   48
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   297978
Seq. No.
                   LIB3150-071-P1-N1-G10
Seq. ID
                   BLASTX
Method
                   g121446
NCBI GI
                   251
BLAST score
                   1.0e-21
E value
                   70
Match length
% identity
                   76
                   FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR
NCBI Description
                   (FD-GOGAT) >gi 100877 pir A38596 glutamate synthase
                   (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190)
                   ferredoxin-dependent glutamate synthase [Zea mays]
                   297979
Seq. No.
                   LIB3150-072-P2-K1-A9
Seq. ID
                   BLASTX
Method
                   g3779021
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
                   87
Match length
                   37
% identity
                   (AC005171) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   297980
Seq. No.
Seq. ID
                   LIB3150-072-P2-K1-D3
                   BLASTX
Method
                   g2191131
NCBI GI
                   209
 BLAST score
                   2.0e-16
 E value
```



```
NCBI Description (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]
                  297981
Seq. No.
                  LIB3150-073-P1-N1-A11
Seq. ID
                  BLASTX
Method
                  g3342821
NCBI GI
BLAST score
                  188
                  2.0e-21
E value
Match length
                  90
                  56
% identity
NCBI Description (AF076954) eukaryotic translation initiation factor small
                  subunit [Zea mays]
                  297982
Seq. No.
                  LIB3150-073-P1-N1-E10
Seq. ID
                  BLASTX
Method
                  g1350720
NCBI GI
BLAST score
                  235
                  8.0e-20
E value
                  73
Match length
                  63
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
                  297983
Seq. No.
                  LIB3150-073-P1-N1-E5
Seq. ID
Method
                  BLASTX
                  q3413700
NCBI GI
BLAST score
                  168
                  2.0e-12
E value
Match length
                  37
                  86
% identity
NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.
                  297984
                  LIB3150-073-P1-N1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1326372
BLAST score
                  153
E value
                  2.0e-10
Match length
                   68
% identity
NCBI Description (U58750) Similar to Histone. [Caenorhabditis elegans]
                   297985
Seq. No.
                  LIB3150-073-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1381676
BLAST score
                   236
                   9.0e-20
E value
                  73
Match length
                   68
% identity
                  (U58853) small GTP-binding protein [Glycine max]
NCBI Description
                   297986
Seq. No.
                   LIB3150-073-P1-N1-G2
Seq. ID
```

BLASTX

g2244834

Method NCBI GI



```
BLAST score
                  1.0e-11
E value
                  41
Match length
                  66
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  297987
Seq. No.
                  LIB3150-073-P1-N1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3608481
                  272
BLAST score
                  3.0e-24
E value
                  68
Match length
                  75
% identity
                  (AF088913) ribosomal protein L27a [Petunia x hybrida]
NCBI Description
                  297988
Seq. No.
                  LIB3150-073-P2-K1-A1
Seq. ID
Method
                  BLASTN
                  g644491
NCBI GI
BLAST score
                  56
E value
                  8.0e-23
Match length
                  152
% identity
                  85
NCBI Description Corn mRNA for elongation factor 1A
                  297989
Seq. No.
                  LIB3150-073-P2-K1-A11
Seq. ID
                  BLASTX
Method
                  g1172816
NCBI GI
                  194
BLAST score
                  7.0e-15
E value
Match length
                  70
                   60
% identity
                  60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395_
NCBI Description
                   (X81799) ribosomal protein L16 [Arabidopsis thaliana]
                   297990
Seq. No.
Seq. ID
                  LIB3150-073-P2-K1-A7
                  BLASTX
Method
                   g136063
NCBI GI
BLAST score
                   261
                   9.0e-23
E value
Match length
                   53
                   100
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >qi 68426 pir ISZMT triose-phosphate isomerase (EC
                   5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
                   isomerase 1 [Zea mays] >gi 217974 dbj BAA00009 (D00012)
                   triosephosphate isomerase [Zea mays]
Seq. No.
                   297991
Seq. ID
                   LIB3150-073-P2-K1-A9
```

Method BLASTX
NCBI GI g1172874
BLAST score 145
E value 5.0e-09



Match length 102 % identity 35

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 297992

Seq. ID LIB3150-073-P2-K1-B10

Method BLASTN
NCBI GI g4185305
BLAST score 43
E value 6.0e-15
Match length 207

% identity 81

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 297993

Seq. ID LIB3150-073-P2-K1-B3

Method BLASTX
NCBI GI g3745759
BLAST score 195
E value 6.0e-15
Match length 56
% identity 70

NCBI Description Chain B, X-Ray Structure Of The Nucleosome Core Particle At

2.8 A Resolution >gi_3745763_pdb_1AOI_F Chain F, X-Ray Structure Of The Nucleosome Core Particle At 2.8 A

Resolution

Seq. No. 297994

Seq. ID LIB3150-073-P2-K1-B8

Method BLASTN
NCBI GI g2286150
BLAST score 263
E value 1.0e-146
Match length 275
% identity 99

NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA,

complete cds

Seq. No. 297995

Seq. ID LIB3150-073-P2-K1-C4

Method BLASTX
NCBI GI g2182029
BLAST score 233
E value 2.0e-19
Match length 89
% identity 57

NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 297996

Seq. ID LIB3150-073-P2-K1-C9



```
BLASTN
Method
NCBI GI
                  g22324
BLAST score
                  71
                  1.0e-31
E value
                  151
Match length
                  87
% identity
                  Z.mays mRNA for H2B histone (clone cH2B221)
NCBI Description
                  297997
Seq. No.
Seq. ID
                  LIB3150-073-P2-K1-F11
                  BLASTN
Method
                  q602605
NCBI GI
                  72
BLAST score
                  3.0e-32
E value
                  254
Match length
                  63
% identity
NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
                  297998
Seq. No.
Seq. ID
                  LIB3150-074-P1-N1-D2
Method
                  BLASTX
NCBI GI
                  q1321661
BLAST score
                  186
                  3.0e-14
E value
                  52
Match length
                  71
% identity
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                  297999
Seq. No.
                  LIB3150-074-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126967
BLAST score
                   358
                  1.0e-34
E value
                  99
Match length
                  14
% identity
                  (AF061807) polyubiquitin [Elaeagnus umbellata]
NCBI Description
                  298000
Seq. No.
Seq. ID
                  LIB3150-074-P1-N1-F12
                  BLASTN
Method
NCBI GI
                   g642120
BLAST score
                   48
                   3.0e-18
E value
                   76
Match length
                   91
% identity
                  Oryza sativa small GTP-binding protein (ORRab-2) mRNA,
NCBI Description
                   complete cds
                   298001
Seq. No.
Seq. ID
                   LIB3150-074-P1-N1-H6
Method
                   BLASTX
NCBI GI
                   g2144183
```

Method BLASTX
NCBI GI g2144183
BLAST score 156
E value 5.0e-11
Match length 53
% identity 53

% identity

93



```
DNA-directed RNA polymerase (EC 2.7.7.6) chain III -
NCBI Description
                  Ecotype Columbia >gi 1184686 (U35049) RNA polymerase I(A)
                  and III(C) 14 kDa subunit [Arabidopsis thaliana]
                  >gi 1184688 (U35050) Arabidopsis thaliana RNA polymerase
                  I(A) and III(C) 14 kDa subunit [Arabidopsis thaliana]
                  >gi 3980382 (AC004561) RNA polymerase I(A) and III(C) 14
                  kDa subunit (AtRPAC14) [Arabidopsis thaliana]
                  298002
Seq. No.
Seq. ID
                  LIB3150-074-P2-K1-G7
                  BLASTN
Method
                  g602605
NCBI GI
                  43
BLAST score
                  5.0e-15
E value
                  75
Match length
                  89
% identity
                  Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
NCBI Description
                  298003
Seq. No.
                  LIB3150-074-P2-K1-H4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g902585
                  67
BLAST score
                  2.0e-29
E value
                  219
Match length
                  83
% identity
                  Zea mays clone MubG9 ubiquitin gene, complete cds
NCBI Description
                  298004
Seq. No.
                  LIB3150-074-P2-K1-H7
Seq. ID
                  BLASTN
Method
                  g393400
NCBI GI
BLAST score
                  71
                  8.0e-32
E value
Match length
                  156
                  85
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
                  298005
Seq. No.
Seq. ID
                  LIB3150-075-P1-N1-D1
                  BLASTX
Method
                  q4588906
NCBI GI
BLAST score
                  195
                  2.0e-15
E value
                  49
Match length
                  80
% identity
                  (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
Seq. No.
                  298006
                  LIB3150-075-P1-N1-E10
Seq. ID
                  BLASTN
Method
NCBI GI
                  q540534
BLAST score
                   58
                   6.0e-24
E value
Match length
                   82
```

41829

NCBI Description Rice mRNA for q group of receptor for activated C-kinase,



complete cds

298007 Seq. No. LIB3150-075-P1-N1-E7 Seq. ID ${\tt BLASTX}$ Method g1184774 NCBI GI 165 BLAST score 2.0e-20 E value 59 Match length 92 % identity (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC3 [Zea mays] 298008 Seq. No. LIB3150-075-P1-N1-F7 Seq. ID BLASTX Method g1053047 NCBI GI 301 BLAST score 1.0e-27 E value 68 Match length 90 % identity (U38425) histone H3 [Glycine max] >gi 1053049 (U38426) NCBI Description histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max] 298009 Seq. No. LIB3150-075-P1-N1-G7 Seq. ID Method BLASTX g729676 NCBI GI 204 BLAST score 2.0e-18 E value 75 Match length 72 % identity HISTONE H3.1 >gi 542444 pir S41499 histone H3.1 -NCBI Description Tetrahymena thermophila (SGC5) >gi 161788 (M87304) histone H3 [Tetrahymena thermophila] >gi_161790 (M87504) histone H3 [Tetrahymena thermophila] 298010 Seq. No. LIB3150-075-P2-N2-A3 Seq. ID BLASTX Method g113621 NCBI GI 332 BLAST score 5.0e-31 E value 67 Match length 97 % identity FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description >gi 68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase

[Zea mays] >gi 295850 emb CAA31366 (X12872) fructose bisphosphate aldolase [Zea mays] >gi 225624 prf 1307278A

cytoplasmic aldolase [Zea mays]

298011 Seq. No.

Seq. ID LIB3150-075-P2-N2-B1

BLASTX Method NCBI GI g2982289



```
BLAST score
                  1.0e-38
E value
                  78
Match length
                  97
% identity
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]
Seq. No.
                  298012
                  LIB3150-075-P2-N2-B3
Seq. ID
                  BLASTN
Method
                  q22272
NCBI GI
BLAST score
                  140
E value
                  6.0e-73
Match length
                  219
                  91
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                  298013
Seq. No.
                  LIB3150-075-P2-N2-D1
Seq. ID
                  BLASTX
Method
                  q2507281
NCBI GI
                  246
BLAST score
                  1.0e-24
E value
Match length
                  66
                  91
% identity
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                   (X97380) atran2 [Arabidopsis thaliana]
                   298014
Seq. No.
                  LIB3150-075-P2-N2-D8
Seq. ID
                  BLASTX
Method
                   q401238
NCBI GI
                   536
BLAST score
                   4.0e-55
E value
Match length
                   131
% identity
                  UBIQUITIN-ACTIVATING ENZYME E1 3 >gi_170686 (M90664)
NCBI Description
                   ubiquitin activating enzyme [Triticum aestivum]
Seq. No.
                   298015
                   LIB3150-075-P2-N2-F2
Seq. ID
                   BLASTN
Method
                   g22100
NCBI GI
                   33
BLAST score
                   3.0e-09
E value
                   57
Match length
                   89
% identity
NCBI Description Z.mays 27kDa zein locus DNA
                   298016
Seq. No.
                   LIB3150-075-P2-N2-H10
Seq. ID
                   BLASTX
Method
                   g4220445
NCBI GI
BLAST score
                   320
                   3.0e-32
E value
Match length
                   132
                   22
% identity
```

NCBI Description (AC006216) Similar to gi 3004555 F19F24.14 salt inducible



protein homolog from Arabidopsis thaliana BAC gb_AC003673. [Arabidopsis thaliana]

 Seq. No.
 298017

 Seq. ID
 LIB3150-075-P2-N2-H11

 Method
 BLASTX

 NCBI GI
 g4220445

BLAST score 171 E value 1.0e-12

Match length 73 % identity 47

NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible

protein homolog from Arabidopsis thaliana BAC gb_AC003673.

[Arabidopsis thaliana]

Seq. No. 298018

Seq. ID LIB3150-075-P2-N2-H12

Method BLASTX
NCBI GI g1730666
BLAST score 169
E value 7.0e-12
Match length 70
% identity 54

NCBI Description HYPOTHETICAL 32.2 KD PROTEIN IN ARE2-SWP73 INTERGENIC

REGION >gi_2131968_pir__S63351 hypothetical protein YNR020c

- yeast (Saccharomyces cerevisiae)

>gi_1302506_emb_CAA96299_ (Z71635) ORF YNR020c

[Saccharomyces cerevisiae]

Seq. No. 298019

Seq. ID LIB3150-076-P1-N1-F3

Method BLASTX
NCBI GI g4582468
BLAST score 150
E value 7.0e-10
Match length 64
% identity 47

NCBI Description (AC007071) putative 40S ribosomal protein; contains

C-terminal domain [Arabidopsis thaliana]

Seq. No. 298020

Seq. ID LIB3150-076-P1-N1-G3

Method BLASTX
NCBI GI g1184776
BLAST score 280
E value 4.0e-25
Match length 71
% identity 79

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 298021

Seq. ID LIB3150-076-P2-N2-A7

Method BLASTX
NCBI GI g3337352
BLAST score 331
E value 4.0e-31



Match length 101 % identity 66 NCBI Description (ACO

(AC004481) putative chromatin structural protein Supt5hp

[Arabidopsis thaliana]

Seq. No. 298022

Seq. ID LIB3150-076-P2-N2-A9

Method BLASTN
NCBI GI g1839582
BLAST score 47
E value 9.0e-18

E value 9.0e-13
Match length 63
% identity 94

NCBI Description polyubiquitin homolog {clone CHEM 6} [Zea mays=maize, cv.

INRA 258, mercuric chloride-treated, leaves, mRNA Partial,

199 nt, segment 1 of 2]

Seq. No. 298023

Seq. ID LIB3150-076-P2-N2-C6

Method BLASTX
NCBI GI g2117937
BLAST score 623
E value 4.0e-65
Match length 123
% identity 94

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi 1212996 emb_CAA62689_ (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No. 298024

Seq. ID LIB3150-076-P2-N2-E8 Method BLASTN

Method BLASTN
NCBI GI g4185305
BLAST score 84
E value 2.0e-39
Match length 304

% identity 83

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 298025

Seq. ID LIB3150-076-P2-N2-F1

Method BLASTX
NCBI GI g1351974
BLAST score 390
E value 8.0e-38
Match length 105
% identity 77

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325

ADP-ribosylation factor - maize >gi_1076789_pir__\$53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 298026

Seq. ID LIB3150-076-P2-N2-G4



```
BLASTN
Method
NCBI GI
                  g22312
                  70
BLAST score
                  4.0e-31
E value
                  97
Match length
                  94
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
                  298027
Seq. No.
                  LIB3150-076-P2-N2-H12
Seq. ID
Method
                  BLASTX
                  q2286153
NCBI GI
                  372
BLAST score
                  9.0e-36
E value
                  75
Match length
% identity
                  100
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  298028
Seq. No.
                  LIB3150-076-P2-N2-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g913865
BLAST score
                  153
                  1.0e-10
E value
Match length
                  49
                  61
% identity
                  branching enzyme II BEII [Zea mays, cultivar B73,
NCBI Description
                  endosperms, Peptide, 738 aa]
                  298029
Seq. No.
                  LIB3150-077-P1-N1-A12
Seq. ID
Method
                  BLASTX
                  g4038471
NCBI GI
                   349
BLAST score
                  5.0e-33
E value
                  86
Match length
                  80
% identity
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
NCBI Description
                   298030
Seq. No.
Seq. ID
                   LIB3150-077-P1-N1-E5
Method
                  BLASTX
                   g417154
NCBI GI
BLAST score
                   168
                   2.0e-18
E value
                   84
Match length
                   79
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
```

Seq. No. 298031

Seq. ID LIB3150-077-P1-N1-E7

Method BLASTX NCBI GI g122022



```
BLAST score
                  8.0e-09
E value
Match length
                  94
                  44
% identity
                  HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat
NCBI Description
                  >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                  aestivum]
                  298032
Seq. No.
                  LIB3150-077-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3294469
BLAST score
                  165
                  2.0e-21
E value
                  101
Match length
                   63
% identity
                  (U89342) phosphoglucomutase 2 [Zea mays]
NCBI Description
                  298033
Seq. No.
                  LIB3150-077-P1-N1-F4
Seq. ID
                  BLASTX
Method
                   q4567275
NCBI GI
BLAST score
                   248
E value
                   8.0e-27
                   108
Match length
% identity
                   61
                  (AC006841) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   298034
Seq. No.
                   LIB3150-077-P1-N1-G3
Seq. ID
                   BLASTN
Method
                   g3015620
NCBI GI
                   55
BLAST score
E value
                   3.0e-22
                   291
Match length
% identity
                   80
                   Zea mays low molecular weight heat shock protein precursor
NCBI Description
                   (hsp22) mRNA, nuclear gene encoding mitochondrial protein,
                   complete cds
                   298035
Seq. No.
                   LIB3150-077-P1-N1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g119355
                   340
BLAST score
                   5.0e-32
E value
                   95
Match length
                   77
% identity
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi 100869_pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi 22273 emb_CAA39454_ (X55981) enolase
                   [Zea mays]
```

Seq. No. Seq. ID LIB3150-077-P2-N2-C4

298036

BLASTN Method

NCBI GI



```
g22272
NCBI GI
                  99
BLAST score
                  2.0e-48
E value
                  205
Match length
                  88
% identity
                  Maize mRNA for enclase (2-phospho-D-glycerate hydrolase)
NCBI Description
                  298037
Seq. No.
                  LIB3150-077-P2-N2-E2
Seq. ID
                  BLASTN
Method
                  g1808693
NCBI GI
                  132
BLAST score
                  5.0e-68
E value
                  224
Match length
                  90
% identity
NCBI Description S.stapfianus pSD.34 mRNA
                  298038
Seq. No.
                  LIB3150-077-P2-N2-E5
Seq. ID
                  BLASTX
Method
                  q118104
NCBI GI
BLAST score
                   547
                   3.0e-56
E value
                   121
Match length
                   87
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi_82914\overline{8}_{emb}CAA48638_{(X68678)} cyclophilin [Zea mays]
                   298039
Seq. No.
                   LIB3150-077-P2-N2-E6
Seq. ID
                   BLASTX
Method
                   g1185556
NCBI GI
                   159
BLAST score
                   2.0e-11
E value
                   37
Match length
                   92
% identity
                  (U45859) glyceraldehyde-3-phosphate dehydrogenase [Zea
NCBI Description
                   mays]
                   298040
Seq. No.
                   LIB3150-077-P2-N2-F9
Seq. ID
                   BLASTN
Method
                   g1037129
NCBI GI
BLAST score
                   191
                   1.0e-103
E value
                   219
Match length
                   65
% identity
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298041
Seq. No.
Seq. ID
                   LIB3150-077-P2-N2-G9
                   BLASTX
Method
```

41836

g2865661



BLAST score 2.0e-09 E value 55 Match length 58 % identity NCBI Description (AF045548) alcohol dehydrogenase 1 [Tripsacum dactyloides] 298042 Seq. No. LIB3150-077-P2-N2-H4 Seq. ID BLASTX Method g2511541 NCBI GI 287 BLAST score 7.0e-26 E value 77 Match length % identity 73 NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa] 298043 Seq. No. LIB3150-078-P1-N1-A8 Seq. ID BLASTX Method

g3334138 NCBI GI 152 BLAST score 2.0e-10 E value Match length 41 63 % identity

NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin

[Glycine max]

298044 Seq. No.

LIB3150-078-P1-N1-B6 Seq. ID

Method BLASTX g1351904 NCBI GI BLAST score 288 2.0e-26 E value 70 Match length 83 % identity

NCBI Description ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST

PRECURSOR (AK-HSDH 1) (AKHSDH1) >gi_500851 (L33912) aspartate kinase-homoserine dehydrogenase [Zea mays]

Seq. No. 298045

LIB3150-078-P1-N1-C1 Seq. ID

Method BLASTX NCBI GI g4218535 BLAST score 211 3.0e-17 E value 79 Match length % identity 58

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

298046 Seq. No.

LIB3150-078-P1-N1-D2 Seq. ID

BLASTX Method g3367522 NCBI GI BLAST score 418 4.0e-41 E value 142 Match length 55 % identity



```
(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  298047
Seq. No.
                  LIB3150-078-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112994
                  321
BLAST score
                  7.0e-30
E value
Match length
                  71
% identity
                  92
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >qi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  298048
Seq. No.
                  LIB3150-078-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432866
BLAST score
                  147
                  2.0e-09
E value
Match length
                  80
                  39
% identity
                   (AC006300) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  298049
Seq. No.
                  LIB3150-078-P1-N1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2282584
                   484
BLAST score
                  7.0e-49
E value
                  104
Match length
                  88
% identity
                  (U76259) elongation factor 1-alpha [Zea mays]
NCBI Description
                   298050
Seq. No.
                   LIB3150-078-P1-N1-G3
Seq. ID
                  BLASTX
Method
                   g112994
NCBI GI
                   427
BLAST score
                   3.0e-42
E value
                   91
Match length
                   93
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi 22313 emb_CAA31077 (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                   mays]
```

Seq. No. 298051

Seq. ID LIB3150-078-P1-N1-H7

Method BLASTN

41838

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```
q303854
NCBI GI
                  54
BLAST score
                  1.0e-21
E value
                  162
Match length
                  85
% identity
NCBI Description Rice mRNA for ribosomal protein L7A, complete cds
                  298052
Seq. No.
                  LIB3150-078-P2-N2-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580398
BLAST score
                  349
E value
                   6.0e - 34
Match length
                   111
                   65
% identity
                   (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                   thaliana]
                   298053
Seq. No.
                   LIB3150-078-P2-N2-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3747050
BLAST score
                   328
E value
                   1.0e-30
                   69
Match length
                   96
% identity
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                   298054
                   LIB3150-078-P2-N2-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3747049
BLAST score
                   35
                   1.0e-10
E value
                   83
Match length
% identity
                   86
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds
                   298055
Seq. No.
                   LIB3150-078-P2-N2-D5
Seq. ID
                   BLASTN
Method
                   g293886
NCBI GI
BLAST score
                   52
                   6.0e-21
E value
                   96
Match length
                   89
% identity
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
NCBI Description
                   end, (clone GAPC3)
                   298056
Seq. No.
Seq. ID
                   LIB3150-078-P2-N2-D8
                   BLASTN
Method
```

NCBI GI g21800 106 BLAST score 1.0e-52 E value Match length 196 % identity 89



NCBI Description T.aestivum L mRNA for histone H2B

Seq. No. 298057

Seq. ID LIB3150-079-P1-N1-A11

Method BLASTX
NCBI GI g113621
BLAST score 163
E value 3.0e-11
Match length 68
% identity 57

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 298058

Seq. ID LIB3150-079-P1-N1-A8

Method BLASTX
NCBI GI g232029
BLAST score 238
E value 3.0e-20
Match length 70
% identity 70

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_100154_pir__S21989 translation elongation factor eEF-1

alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)

elongation factor 1A [Daucus carota]

Seq. No. 298059

Seq. ID LIB3150-079-P1-N1-D2

Method BLASTX
NCBI GI g2760349
BLAST score 232
E value 9.0e-20
Match length 68
% identity 14

NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]

Seq. No. 298060

Seq. ID LIB3150-079-P1-N1-E2

Method BLASTX
NCBI GI g1184776
BLAST score 405
E value 2.0e-39
Match length 78
% identity 95

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 298061

Seq. ID LIB3150-079-P1-N1-E3

Method BLASTX
NCBI GI g4510368
BLAST score 276
E value 2.0e-24



Match length 131 % identity 56

NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis

thaliana]

Seq. No. 298062

Seq. ID LIB3150-079-P1-N1-E7

Method BLASTX
NCBI GI g730558
BLAST score 225
E value 6.0e-28
Match length 96
% identity 74

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal

protein L34 - common tobacco >gi_2129964_pir_S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34

[Nicotiana tabacum]

Seq. No. 298063

Seq. ID LIB3150-079-P2-N2-A11

Method BLASTN
NCBI GI g3318612
BLAST score 78
E value 6.0e-36
Match length 190
% identity 84

NCBI Description Zea mays mRNA for mitochondrial phosphate transporter,

complete cds

Seq. No. 298064

Seq. ID LIB3150-079-P2-N2-B1

Method BLASTN
NCBI GI g416263
BLAST score 37
E value 2.0e-11
Match length 65
% identity 89

NCBI Description Rice mRNA for ribosomal protein S28, partial sequence

Seq. No. 298065

Seq. ID LIB3150-079-P2-N2-E4

Method BLASTN
NCBI GI g1213278
BLAST score 60
E value 3.0e-25
Match length 100
% identity 90

NCBI Description Z.mays ZEMb gene

Seq. No. 298066

Seq. ID LIB3150-079-P2-N2-F3

Method BLASTX
NCBI GI g3805847
BLAST score 315
E value 5.0e-29



```
Match length
                  111
                  58
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  298067
                  LIB3150-079-P2-N2-H5
Seq. ID
                  BLASTN
Method
                  q886739
NCBI GI
                  70
BLAST score
                  3.0e-31
E value
                  245
Match length
% identity
                  84
NCBI Description Z.mays histone H4 gene
```

Seq. No. LIB3150-080-P2-N2-G2 Seq. ID Method BLASTN g1550813 NCBI GI

BLAST score 102 3.0e-50 E value Match length 181 % identity 90

NCBI Description Z.mays mRNA for acidic ribosomal protein PO

298069 Seq. No. Seq. ID

LIB3150-081-P1-N1-C6

Method BLASTX NCBI GI q2137285 BLAST score 145 4.0e-09 E value 75 Match length 40 % identity

NCBI Description estrogen-responsive finger protein - mouse

>gi 1088467_dbj_BAA09941_ (D63902) estrogen-responsive

finger protein [Mus musculus]

298070 Seq. No.

LIB3150-081-P1-N1-E1 Seq. ID

BLASTX Method g425194 NCBI GI 448 BLAST score 9.0e-45 E value 87 Match length 99 % identity

(L26243) heat shock protein [Spinacia oleracea] >gi 2660772 NCBI Description

(AF034618) cytosolic heat shock 70 protein [Spinacia

oleracea]

298071 Seq. No.

LIB3150-081-P1-N1-G2 Seq. ID

BLASTX Method g3913804 NCBI GI BLAST score 260 1.0e-22 E value 65 Match length 83 % identity

NCBI Description HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone



[Zea mays]

```
298072
Seq. No.
                  LIB3150-081-P1-N1-H3
Seq. ID
                  BLASTX
Method
                  q118104
NCBI GI
                  477
BLAST score
                  4.0e-48
E value
                   98
Match length
                   91
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                                 _CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   >gi_68408_pir_
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                   >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   298073
Seq. No.
                   LIB3150-081-P2-N2-D11
Seq. ID
                   BLASTN
Method
                   g168425
NCBI GI
                   186
BLAST score
                   1.0e-100
E value
                   255
Match length
                   93
% identity
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                   298074
Seq. No.
                   LIB3150-081-P2-N2-F8
Seq. ID
                   BLASTX
Method
                   q520544
NCBI GI
                   251
BLAST score
                   1.0e-21
E value
                   46
Match length
                   96
% identity
                  (U12195) betaine aldehyde dehydrogenase [Sorghum bicolor]
NCBI Description
                   298075
Seq. No.
                   LIB3150-082-P1-N1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q168586
                   147
BLAST score
                   7.0e-10
E value
                   43
Match length
                   70
% identity
NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]
                   298076
Seq. No.
                   LIB3150-082-P1-N1-B8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2811133
                   100
 BLAST score
                   4.0e-49
 E value
                   189
Match length
                   88
 % identity
                   Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
 NCBI Description
                   partial cds
```

```
298077
Seq. No.
Seq. ID
                  LIB3150-082-P1-N1-C4
                  BLASTX
Method
                  g168407
NCBI GI
BLAST score
                  173
                  2.0e-12
E value
                  57
Match length
                  70
% identity
                  (M32984) alcohol dehydrogenase [Zea mays]
NCBI Description
                  298078
Seq. No.
                  LIB3150-082-P2-N2-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g829147
BLAST score
                  44
                  5.0e-16
E value
Match length
                  56
% identity
                  95
NCBI Description Z.mays gene for cyclophilin
                  298079
Seq. No.
Seq. ID
                  LIB3150-083-P1-N1-A1
Method
                  BLASTN
NCBI GI
                  q1143704
BLAST score
                  97
                  3.0e-47
E value
Match length
                  125
% identity
                  94
NCBI Description Z.mays mRNA for homeobox 2a protein
                  298080
Seq. No.
Seq. ID
                  LIB3150-083-P1-N1-A2
Method
                  BLASTX
                  g126896
NCBI GI
BLAST score
                  340
                  1.0e-37
E value
                  93
Match length
                  86
% identity
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)
                  precursor, mitochondrial - watermelon
                  >gi 18297_emb_CAA35239 (X17362) precursor protein (AA -27
                  to 320) [Citrullus lanatus]
Seq. No.
                  298081
Seq. ID
                  LIB3150-083-P1-N1-B3
                  BLASTX
Method
NCBI GI
                  q4206112
BLAST score
                  175
                  3.0e-13
E value
```

Match length 71 61 % identity

(AF097662) alpha tubulin [Mesembryanthemum crystallinum] NCBI Description

Seq. No. 298082

Seq. ID LIB3150-083-P1-N1-B5

Method BLASTX



```
q4206112
NCBI GI
                  159
BLAST score
                  2.0e-11
E value
                  59
Match length
                  59
% identity
NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]
                  298083
Seq. No.
                  LIB3150-083-P1-N1-C1
Seq. ID
Method
                  BLASTX
                  g1279206
NCBI GI
BLAST score
                  190
                  1.0e-14
E value
Match length
                  68
                  62
% identity
NCBI Description (X97446) alpha-tubulin [Avena sativa]
                  298084
Seq. No.
                  LIB3150-083-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1883028
                  231
BLAST score
E value
                  2.0e-19
Match length
                  72
% identity
NCBI Description (X91511) histone H4 [Diprion pini]
                  298085
Seq. No.
                  LIB3150-083-P1-N1-F2
Seq. ID
Method
                  BLASTN
                   g577824
NCBI GI
BLAST score
                   146
E value
                   1.0e-76
                   170
Match length
% identity
                   96
NCBI Description Z.mays gene for H2B histone (gH2B3)
                   298086
Seq. No.
                   LIB3150-083-P1-N1-G4
Seq. ID
                   BLASTX
Method
                   g3935184
NCBI GI
                   384
BLAST score
                   3.0e-37
E value
                   115
Match length
                   65
% identity
NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]
                   298087
Seq. No.
                   LIB3150-083-P1-N1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3122071
BLAST score
                   304
E value
                   4.0e-28
                   62
Match length
                   95
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
```

>gi_2130148_pir__S66339 translation elongation factor eEF-1



alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408) alpha subunit of tlanslation elongation factor 1 [Zea mays]

298088 Seq. No. LIB3150-083-P2-N2-A10 Seq. ID Method BLASTX g4406372 NCBI GI BLAST score 188 E value 3.0e-14 Match length 43 % identity 77 (AF109156) thiosulfate sulfurtransferase [Datisca NCBI Description glomerata] 298089 Seq. No. LIB3150-083-P2-N2-C12 Seq. ID Method BLASTN NCBI GI g1575127 BLAST score 220 1.0e-120 E value 280 Match length 94 % identity NCBI Description Zea mays lumenal binding protein cBiPe2 mRNA, complete cds 298090 Seq. No. LIB3150-083-P2-N2-D11 Seq. ID Method BLASTN NCBI GI q531055 BLAST score 64 E value 1.0e-27 72 Match length 97 % identity NCBI Description Wheat mRNA for protein H2B-6, complete cds Seq. No. 298091 LIB3150-083-P2-N2-F12 Seq. ID BLASTX Method q2760321 NCBI GI BLAST score 309 2.0e-28 E value 108 Match length 59 % identity (AC002130) F1N21.6 [Arabidopsis thaliana] NCBI Description 298092 Seq. No. LIB3150-083-P2-N2-G11 Seq. ID BLASTX Method g480450 NCBI GI BLAST score 158 1.0e-10 E value 34 Match length

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi 402552_emb_CAA49506_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 298093

% identity

91



Seq. ID LIB3150-083-P2-N2-H5

Method BLASTN
NCBI GI g2642323
BLAST score 89
E value 2.0e-42
Match length 222
% identity 86

NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 298094

Seq. ID LIB3150-084-P2-N2-F6

Method BLASTN
NCBI GI g498772
BLAST score 39
E value 1.0e-12
Match length 67
% identity 91

NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No. 298095

Seq. ID LIB3150-084-P2-N2-G10

Method BLASTX
NCBI GI g1335862
BLAST score 403
E value 2.0e-39
Match length 88
% identity 86

NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 298096

Seq. ID LIB3150-085-P1-N1-B3

Method BLASTX
NCBI GI g312179
BLAST score 264
E value 2.0e-33
Match length 81
% identity 95

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 298097

Seq. ID LIB3150-085-P1-N1-D2

Method BLASTX
NCBI GI g2624328
BLAST score 207
E value 2.0e-16
Match length 63
% identity 65

NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

Seq. No. 298098

Seq. ID LIB3150-085-P1-N1-F1

Method BLASTX NCBI GI g1172833



BLAST score 249 E value 1.0e-21 Match length 58 % identity 86

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi 495729 (L16789) small

ras-related protein [Arabidopsis thalīana]

>gi_2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis

thaliana]

Seq. No. 298099

Seq. ID LIB3150-085-P1-N1-G1

Method BLASTN
NCBI GI g4099507
BLAST score 66
E value 6.0e-29
Match length 141
% identity 87

NCBI Description Zea mays proliferating cell nuclear antigen (ZmPCNA2) mRNA,

complete cds

Seq. No. 298100

Seq. ID LIB3150-085-P1-N1-G2

Method BLASTX
NCBI GI g1262171
BLAST score 203
E value 6.0e-16
Match length 61
% identity 72

NCBI Description (U21557) phosphoprotein phosphatase 2A, regulatory subunit

A [Arabidopsis thaliana]

Seq. No. 298101

Seq. ID LIB3150-086-P1-N1-C1

Method BLASTX
NCBI GI g3024018
BLAST score 165
E value 5.0e-12
Match length 38
% identity 87

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 298102

Seq. ID LIB3150-086-P1-N1-D4

Method BLASTN
NCBI GI g168484
BLAST score 50
E value 1.0e-19
Match length 114
% identity 86

NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298103

Seq. ID LIB3150-086-P1-N1-E8

Method BLASTX



```
NCBI GI
                  q1184776
BLAST score
                  293
                  2.0e-26
E value
Match length
                  63
                  90
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
                  298104
Seq. No.
Seq. ID
                  LIB3150-087-P2-K1-C3
Method
                  BLASTN
NCBI GI
                  q498774
BLAST score
                  74
                  9.0e-34
E value
                  197
Match length
                  85
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein
                  298105
Seq. No.
                  LIB3150-087-P2-K1-D6
Seq. ID
Method
                  BLASTN
                  q927571
NCBI GI
BLAST score
                  51
E value
                  2.0e-20
                  62
Match length
                  97
% identity
NCBI Description Z.mays mRNA for calreticulin precursor
Seq. No.
                  298106
                  LIB3150-087-P2-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g861170
BLAST score
                  298
                   5.0e-27
E value
Match length
                   76
% identity
                   78
NCBI Description (X03697) heat shock protein 70 [Zea mays]
Seq. No.
                  298107
                  LIB3150-087-P2-K1-F1
Seq. ID
                  BLASTN
Method
                   g22516
NCBI GI
BLAST score
                   114
E value
                   2.0e-57
                  198
Match length
                   89
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298108
Seq. No.
Seq. ID
                   LIB3150-087-P2-K1-F11
                   BLASTN
Method
NCBI GI
                   g2282583
BLAST score
                   38
                   6.0e-12
E value
Match length
                   134
                   83
% identity
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete
```



```
298109
Seq. No.
Seq. ID
                  LIB3150-087-P2-K1-G2
Method
                  BLASTN
                  g22121
NCBI GI
BLAST score
                  191
                  1.0e-103
E value
                  243
Match length
                   95
% identity
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)
Seq. No.
                  298110
                  LIB3150-088-P2-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                   q22272
BLAST score
                   105
                   7.0e-52
E value
Match length
                   328
                   82
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.
                   298111
                   LIB3150-088-P2-K1-B10
Seq. ID
Method
                   BLASTX
                   g3928086
NCBI GI
BLAST score
                   157
E value
                   2.0e-10
                   45
Match length
% identity
                   58
                  (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   298112
Seq. ID
                   LIB3150-088-P2-K1-D11
Method
                   BLASTX
NCBI GI
                   g4586035
BLAST score
                   147
                   3.0e-10
E value
                   89
Match length
                   48
% identity
                   (AC007109) putative prohibitin protein [Arabidopsis
NCBI Description
                   thaliana]
                   298113
Seq. No.
Seq. ID
                   LIB3150-088-P2-K1-F2
Method
                   BLASTX
NCBI GI
                   q4115937
BLAST score
                   226
                   2.0e-18
E value
                   51
Match length
                   75
% identity
                   (AF118223) contains similarity to human PCF11p homolog
NCBI Description
                   (GB:AF046935) [Arabidopsis thaliana]
```

298114

BLASTX

LIB3150-089-P1-N1-B10

Seq. No. Seq. ID

Method



```
q417154
NCBI GI
BLAST score
                  316
                  2.0e-29
E value
                  76
Match length
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  -
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  298115
Seq. No.
                  LIB3150-089-P1-N1-B2
Seq. ID
Method
                  BLASTX
                  q417154
NCBI GI
                  288
BLAST score
                  5.0e-30
E value
Match length
                  104
                  71
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                  298116
                  LIB3150-089-P1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129626
                   360
BLAST score
                  2.0e-34
E value
Match length
                   88
                   76
% identity
                  J-domain protein - Arabidopsis thaliana
NCBI Description
                   >gi 928936 emb_CAA89204_ (Z49238) J-domain protein
                   [Arabidopsis thaliana] >gi 1585434 prf__2124427A diamide
                   resistance gene [Arabidopsis thaliana]
Seq. No.
                   298117
                   LIB3150-089-P1-N1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3355475
BLAST score
                   177
                   6.0e-13
E value
                   81
Match length
                   53
% identity
                  (AC004218) ribosomal protein L23a [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   298118
                   LIB3150-089-P1-N1-H2
Seq. ID
                   BLASTN
Method
                   q2623247
NCBI GI
                   51
BLAST score
                   3.0e-20
E value
                   107
Match length
                   88
% identity
                  Zea mays SU1 isoamylase (sugary1) gene, complete cds
NCBI Description
```

298119

Seq. No.

```
LIB3150-089-P1-N1-H6
Seq. ID
Method
                  BLASTX
                  q1711036
NCBI GI
BLAST score
                  264
                  3.0e-23
E value
Match length
                  95
% identity
                  (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
NCBI Description
                  sativum]
Seq. No.
                  298120
Seq. ID
                  LIB3150-089-P2-K1-A5
Method
                  BLASTN
NCBI GI
                  q3318612
                  162
BLAST score
                   6.0e-86
E value
                  223
Match length
% identity
                  Zea mays mRNA for mitochondrial phosphate transporter,
NCBI Description
                   complete cds
                   298121
Seq. No.
Seq. ID
                  LIB3150-089-P2-K1-B5
Method
                   BLASTN
                   q342631
NCBI GI
                   56
BLAST score
                   9.0e-23
E value
                   175
Match length
% identity
NCBI Description Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds
                   298122
Seq. No.
                   LIB3150-089-P2-K1-G11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168581
BLAST score
                   79
                   2.0e-36
E value
                   221
Match length
% identity
                   85
                   Z.mays pyruvate, orthophosphate dikinase (PPDK2) gene, 3'
NCBI Description
                   end
                   298123
Seq. No.
                   LIB3150-090-P2-K1-C11
Seq. ID
                   BLASTN
Method
                   g602252
NCBI GI
                   89
BLAST score
                   1.0e-42
E value
                   141
Match length
                   91
% identity
NCBI Description Zea mays enolase (eno2) mRNA, complete cds
                   298124
Seq. No.
                   LIB3150-090-P2-K1-C3
Seq. ID
                   BLASTN
Method
```

q2642323

205

NCBI GI BLAST score

NCBI Description



```
E value
                   1.0e-111
Match length
                   297
% identity
                   93
NCBI Description
                  Zea mays profilin (PRO4) mRNA, complete cds
                   298125
Seq. No.
                   LIB3150-090-P2-K1-D4
Seq. ID
Method
                   BLASTX
                   g4490708
NCBI GI
BLAST score
                   166
                   2.0e-11
E value
Match length
                   56
% identity
                   57
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   298126
Seq. No.
                   LIB3150-091-P1-N1-A4
Seq. ID
                   BLASTX
Method
                   g22166
NCBI GI
BLAST score
                   212
E value
                   4.0e-23
Match length
                   89
                   71
% identity
                  (X15711) adenine nucleotide translocator [Zea mays]
NCBI Description
                   298127
Seq. No.
Seq. ID
                   LIB3150-091-P1-N1-A8
Method
                   BLASTX
NCBI GI
                   g451193
BLAST score
                   204
                   4.0e-16
E value
Match length
                   52
% identity
                   81
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                   >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   298128
Seq. ID
                   LIB3150-091-P1-N1-B10
                   BLASTN
Method
NCBI GI
                   g5091496
BLAST score
                   40
E value
                   3.0e-13
Match length
                   166
 % identity
                   82
                   Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   298129
Seq. No.
                   LIB3150-091-P1-N1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3355620
BLAST score
                   165
E value
                   2.0e-11
Match length
                   40
                   85
 % identity
```

41853

phosphoribosylformylglycinamidine synthase [Hordeum

(AJ000235) partial sequence, homology to



vulgare]

298130 Seq. No. LIB3150-091-P1-N1-F1 Seq. ID BLASTN Method q2431768 NCBI GI BLAST score 64 2.0e-27 E value 160 Match length 85 % identity NCBI Description Zea mays acidic ribosomal protein Pla (rppla) mRNA, complete cds 298131 Seq. No. LIB3150-091-P1-N1-G4 Seq. ID BLASTX Method g3236242 NCBI GI 176 BLAST score 8.0e-13 E value 100 Match length 45 % identity (ACO04684) putative ribosomal protein L36 [Arabidopsis NCBI Description thaliana] Seq. No. 298132 LIB3150-091-P1-N1-G7 Seq. ID BLASTX Method g1174613 NCBI GI 162 BLAST score 1.0e-14 E value 84 Match length 57 % identity 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa] Seq. No. 298133 LIB3150-092-P1-N1-B1 Seq. ID Method BLASTX q462243 NCBI GI 208 BLAST score 1.0e-16 E value 85 Match length % identity HISTONE H4 >gi 421921_pir__S32769 histone H4 - tomato NCBI Description >gi_297150_emb_CAA48923_ (X69179) histone H4 [Lycopersicon esculentum] >gi_297152_emb_CAA48924_ (X69180) histone H4 [Lycopersicon esculentum] >gi_2746721 (AF038387) histone H4

[Capsicum annuum]

Seq. No.

Seq. ID LIB3150-092-P1-N1-B4

298134

Method BLASTX
NCBI GI g461498
BLAST score 227
E value 8.0e-19

```
Match length
                  58
% identity
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                  (ALAAT-2) >gi 320619 pir__S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi 296204_emb_CAA49199_ (X69421)
                  alanine aminotransferase [Panicum miliaceum]
                  298135
Seq. No.
                  LIB3150-092-P1-N1-C3
Seq. ID
                  BLASTX
Method
                  q627584
NCBI GI
                  168
BLAST score
                  6.0e-12
E value
                  114
Match length
                  34
% identity
                  protein p84 - human >gi_550058 (L36529) protein p84 [Homo
NCBI Description
                  sapiens]
                  298136
Seq. No.
                  LIB3150-092-P1-N1-D8
Seq. ID
                  BLASTX
Method
                  g1174867
NCBI GI
                  151
BLAST score
                  1.0e-11
E value
                   71
Match length
                   58
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
NCBI Description
                   PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                   KD PROTEIN) >gi 633687 emb CAA55862 (X79275)
                   ubiquinol--cytochrome c reductase [Solanum tuberosum]
                   >gi 1094912 prf 2107179A cytochrome c
                   oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
                   298137
Seq. No.
                   LIB3150-092-P2-K1-A4
Seq. ID
Method
                   BLASTN
                   q168492
NCBI GI
                   35
BLAST score
E value
                   3.0e-10
                   39
Match length
                   97
 % identity
NCBI Description Corn histone H3 (H3C3) gene, complete cds
 Seq. No.
                   298138
                   LIB3150-092-P2-K1-D12
 Seq. ID
                   BLASTN
 Method
                   g1321660
 NCBI GI
 BLAST score
                   47
                   2.0e-17
 E value
 Match length
                   71
                   92
 % identity
 NCBI Description Rice mRNA for ascorbate peroxidase, complete cds
```

298139

BLASTN

LIB3150-092-P2-K1-E1

Seq. No.

Seq. ID

Method



```
q747916
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
                   124
Match length
                   85
% identity
NCBI Description Z.mays CaM2 mRNA for calmodulin
                   298140
Seq. No.
                   LIB3150-093-P1-N1-A3
Seq. ID
                   BLASTX
Method
                   q3163946
NCBI GI
                   179
BLAST score
                   2.0e-13
E value
Match length
                   50
                   70
% identity
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
                   298141
Seq. No.
                   LIB3150-093-P1-N1-A7
Seq. ID
                   BLASTX
Method
                   g3024018
NCBI GI
                   166
BLAST score
                    1.0e-11
E value
                    89
Match length
% identity
                    42
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                    >gi_1546919_emb_CAA69225_ (Y07920) translation initiation
factor 5A [Zea mays] >gi_2668738 (AF034943) translation
                    initiation factor 5A [Zea mays]
                    298142
Seq. No.
                    LIB3150-093-P1-N1-A8
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2224897
                    211
BLAST score
E value
                    3.0e-17
Match length
                    68
                    56
% identity
NCBI Description (U67132) DNA-binding protein PcMYB1 [Petroselinum crispum]
                    298143
Seq. No.
                    LIB3150-093-P1-N1-F1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g113622
BLAST score
                    268
                    3.0e-41
E value
                    106
Match length
                    92
 % identity
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                    >gi 68197_pir__ADRZY fructose-bisphosphate aldolase (EC
                    4.1.2.13), cytosolic - rice >gi_20204_emb_CAA37290
                    (X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza
                    sativa]
 Seq. No.
                    298144
                    LIB3150-093-P1-N1-G2
 Seq. ID
```

BLASTN

Method

Seq. ID

Method

```
q4151124
 NCBI GI
 BLAST score
                    58
                    4.0e-24
 E value
                    78
 Match length
                    94
% identity
 NCBI Description Zea mays PDI-like protein mRNA, complete cds
                    298145
 Seq. No.
                    LIB3150-093-P1-N1-H2
 Seq. ID
                                                                           4-1
                    BLASTX
 Method
                    q1085973
 NCBI GI
                     191
 BLAST score
                     6.0e-15
 E value
 Match length
 % identity
                     isopentyl pyrophosphate isomerase - Clarkia breweri
(fragment) >gi_572635_emb_CAA57947_ (X82627) isopentenyl
 NCBI Description
                     pyrophosphate isomerase [Clarkia breweri]
                     298146
 Seq. No.
                     LIB3150-093-P1-N1-H4
 Seq. ID
                     BLASTN
 Method
                     g22144
 NCBI GI
 BLAST score
                     180
                     8.0e-97
 E value
                     205
 Match length
                     96
  % identity
                     Maize anaerobically regulated gene for fructose
  NCBI Description
                     bisphosphate aldolase (EC 4.1.2.13)
  Seq. No.
                     298147
                     LIB3150-093-P1-N1-H5
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q461498
                     297
  BLAST score
  E value
                     3.0e-27
                     78
  Match length
                     79
  % identity
                     ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
  NCBI Description
                     TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                      (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                     2.6.1.2) - proso millet \overline{>}gi_296204_emb_CAA49199_ (X69421)
                     alanine aminotransferase [Panicum miliaceum]
  Seq. No.
                     298148
                     LIB3150-093-P2-K1-C10
  Seq. ID
                     BLASTN
  Method
                     g1154858
  NCBI GI
  BLAST score
                      45
                      4.0e-16
  E value
                      145
  Match length
                      82
  % identity
  NCBI Description H.vulgare mRNA for L24 ribosomal protein
                      298149
  Seq. No.
```

41857

LIB3150-093-P2-K1-F2

BLASTX

```
g3885884
NCBI GI
BLAST score
                  211
                  6.0e-17
E value
                  45
Match length
                  89
% identity
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                  298150
Seq. No.
                  LIB3150-094-P1-N1-C5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22272
BLAST score
                   41
E value
                   5.0e-14
                   65
Match length
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                   298151
Seq. No.
                   LIB3150-094-P1-N1-C8
Seq. ID
                   BLASTX
Method
                   q1351014
NCBI GI
                   205
BLAST score
                   3.0e-16
E value
Match length
                   91
                   54
% identity
                   40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
NCBI Description
                   ribosomal protein S8 [Oryza sativa]
                   298152
Seq. No.
                   LIB3150-094-P1-N1-D6
Seq. ID
                   BLASTX
Method
                   g4469020
NCBI GI
                   180
BLAST score
E value
                   2.0e-13
                   66
Match length
% identity
                   48
                   (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   298153
 Seq. No.
                   LIB3150-094-P1-N1-F2
 Seq. ID
Method
                   BLASTX
                   g4115918
NCBI GI
                   200
BLAST score
                   1.0e-15
 E value
                   44
Match length
 % identity
                    (AF118222) similar to nascent polypeptide associated
 NCBI Description
                   complex alpha chain [Arabidopsis thaliana]
                   298154
 Seq. No.
                   LIB3150-094-P1-N1-F8
 Seq. ID
                   BLASTX
 Method
                    g4539437
 NCBI GI
                    345
 BLAST score
                    1.0e-35
 E value
```

122

Match length

Seq. No.

Seq. ID

Method

298160

BLASTX

LIB3150-094-P2-K1-E12



% identity NCBI Description (AL049523) putative protein [Arabidopsis thaliana] 298155 Seq. No. LIB3150-094-P1-N1-G12 Seq. ID Method BLASTX NCBI GI q1332579 BLAST score 492 E value 9.0e-50 Match length 132 % identity NCBI Description (X98063) polyubiquitin [Pinus sylvestris] Seq. No. 298156 LIB3150-094-P1-N1-G7 Seq. ID Method BLASTN NCBI GI g2282583 BLAST score 38 E value 4.0e-12 Match length 106 % identity 84 NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds Seq. No. 298157 Seq. ID LIB3150-094-P2-K1-C12 Method BLASTX NCBI GI g3128181 BLAST score 157 E value 2.0e-10 Match length 51 % identity 61 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana] Seq. No. 298158 LIB3150-094-P2-K1-C2 Seq. ID Method BLASTN NCBI GI g22516 BLAST score 57 E value 1.0e-23 Match length 109 88 % identity NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2) Seq. No. 298159 LIB3150-094-P2-K1-E11 Seq. ID Method BLASTN NCBI GI q312180 BLAST score 73 E value 6.0e-33 Match length 125 % identity 90 NCBI Description Z.mays GapC4 gene



```
NCBI GI
                  g121296
BLAST score
                  362
                  1.0e-34
E value
Match length
                  109
% identity
                  60
                  1,4-ALPHA-GLUCAN BRANCHING ENZYME (GLYCOGEN BRANCHING
NCBI Description
                  ENZYME) >gi 66573 pir NQECA 1,4-alpha-glucan branching
                  enzyme (EC 2.4.1.18) - Escherichia coli >gi_146142 (M13751)
                  branching enzyme (EC 2.4.1.18) [Escherichia coli]
                  >gi_1789839 (AE000419) 1,4-alpha-glucan branching enzyme
                  [Escherichia coli]
Seq. No.
                  298161
                  LIB3150-094-P2-K1-G8
Seq. ID
Method
                  BLASTX
                  a2583123
NCBI GI
BLAST score
                  226
E value
                  1.0e-18
Match length
                  47
% identity
                  83
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  298162
Seq. ID
                  LIB3150-095-P1-N1-A1
Method
                  BLASTX
                  g3738257
NCBI GI
BLAST score
                  168
                  2.0e-12
E value
Match length
                  46
                  78
% identity
NCBI Description
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
                  nigra]
                  298163
Seq. No.
Seq. ID
                  LIB3150-095-P1-N1-B5
                  BLASTX
Method
NCBI GI
                  g2851508
BLAST score
                  327
E value
                  2.0e-30
Match length
                  87
% identity
                  70
                  60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
NCBI Description
                  ribosomal protein L21 (gb L38826). ESTs
                  qb AA395597,qb ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi 3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                  298164
Seq. ID
                  LIB3150-095-P1-N1-C2
Method
                  BLASTX
NCBI GI
                  q4432819
BLAST score
                  153
E value
                  1.0e-10
Match length
                  48
% identity
                  62
```

NCBI Description (AC006593) putative kinesin light chain [Arabidopsis



thaliana]

298165 Seq. No. LIB3150-095-P1-N1-D1 Seq. ID BLASTX Method g122085 NCBI GI BLAST score 455 E value 2.0e-45 109 Match length 85 % identity NCBI Description

HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi 82482 pir S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 $(M3\overline{5}388)$ histone H3 [Zea mays] $>gi_169\overline{6}55$ $(M7\overline{7}493)$ histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi 1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >g \overline{i} 225459 prf $_{-}$ 1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

 Seq. No.
 298166

 Seq. ID
 LIB3150-095-P1-N1-D3

 Method
 BLASTN

 NCBI GI
 g1421729

 BLAST score
 38

BLAST score 38
E value 6.0e-12
Match length 110
% identity 84

NCBI Description Zea mays T cytoplasm male sterility restorer factor 2 (rf2)

mRNA, complete cds

Seq. No. 298167

Seq. ID LIB3150-095-P1-N1-E1

Method BLASTN
NCBI GI g1037129
BLAST score 296
E value 1.0e-166
Match length 400
% identity 94

NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,

Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. Seq. ID

Method



```
298168
Seq. No.
                  LIB3150-095-P1-N1-E12
Seq. ID
                  BLASTX
Method
                  q419803
NCBI GI
                  249
BLAST score
                  1.0e-21
E value
                  69
Match length
                  68
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  298169
Seq. No.
                  LIB3150-095-P2-K1-A7
Seq. ID
                  BLASTN
Method
                  q1154858
NCBI GI
                  45
BLAST score
                  2.0e-16
E value
Match length
                   57
% identity
NCBI Description H.vulgare mRNA for L24 ribosomal protein
                   298170
Seq. No.
                   LIB3150-095-P2-K1-H12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2341060
                   270
BLAST score
E value
                   1.0e-150
                   314
Match length
% identity
                   96
                   Zea mays translational initiation factor eIF-4A (tif-4A3)
NCBI Description
                   mRNA, complete cds
                   298171
Seq. No.
                   LIB3150-096-P1-N1-D10
Seq. ID
Method
                   BLASTX
                   q99771
NCBI GI
                   335
BLAST score
                   2.0e-31
E value
Match length
                   109
% identity
                   66
                   ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana
NCBI Description
                   >gi_166934 (J05539) ubiquitin extension protein (UBQ5)
                   [Arabidopsis thaliana]
                   298172
Seq. No.
                   LIB3150-096-P1-N1-D2
Seq. ID
                   BLASTX
Method
                   g22168
NCBI GI
                   231
BLAST score
                   9.0e-20
E value
                   62
Match length
                   76
 % identity
                   (X15712) adenine nucleotide translocator [Zea mays]
NCBI Description
                   298173
```

41862

LIB3150-096-P1-N1-D3

BLASTX

```
g1136122
NCBI GI
BLAST score
                  496
E value
                  2.0e-50
Match length
                  119
% identity
                  79
                  (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                  298174
Seq. No.
                  LIB3150-096-P1-N1-E1
Seq. ID
                  BLASTX
Method
                  g3925363
NCBI GI
                  157
BLAST score
E value
                  1.0e-10
Match length
                  94
                  46
% identity
NCBI Description
                  (AF067961) homeodomain protein [Malus domestica]
                  298175
Seq. No.
                  LIB3150-096-P1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1723669
BLAST score
                  153
E value
                  5.0e-10
Match length
                  78
% identity
                  41
                  HYPOTHETICAL 71.3 KD PROTEIN IN SCM4-MUP1 INTERGENIC REGION
NCBI Description
                  >gi_2131657_pir__S64348 hypothetical protein YGR054w -
                  yeast (Saccharomyces cerevisiae) >gi 1323065 emb CAA97054
                  (Z72839) ORF YGR054w [Saccharomyces cerevisiae]
                  298176
Seq. No.
Seq. ID
                  LIB3150-096-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  g2505940
BLAST score
                  172
E value
                  2.0e-12
                  65
Match length
                  58
% identity
NCBI Description
                  (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
Seq. No.
                  298177
Seq. ID
                  LIB3150-097-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  g312179
BLAST score
                  386
                  2.0e-37
E value
Match length
                  86
                  87
% identity
NCBI Description
                  (X73151) glyceraldehyde 3-phosphate dehydrogenase
                  (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                  >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays]
```

BLASTN

LIB3150-097-P1-N1-E7

Seq. No. Seq. ID

Method



```
NCBI GI
                  q22292
BLAST score
                  50
E value
                  4.0e-19
Match length
                  82
                  91
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                  298179
                  LIB3150-097-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129946
BLAST score
                  346
E value
                  1.0e-32
                  87
Match length
% identity
                  80
                  ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
NCBI Description
                  common tobacco (fragment) >gi 1184987 (U46927) NTGB1
                  [Nicotiana tabacum]
                  298180
Seq. No.
Seq. ID
                  LIB3150-097-P1-N1-F7
Method
                  BLASTX
                  g1703374
NCBI GI
BLAST score
                  199
                  2.0e-15
E value
Match length
                  72
                  67
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi 2129457 pir S66337
NCBI Description
                  ADP-ribosylation factor 1 - Chlamydomonas reinhardtii
                  >gi 861205 (U27120) ADP-ribosylation factor [Chlamydomonas
                  reinhardtii]
Seq. No.
                  298181
Seq. ID
                  LIB3150-097-P1-N1-F9
Method
                  BLASTX
NCBI GI
                  g1184774
BLAST score
                  232
                  2.0e-26
E value
Match length
                  103
% identity
                  69
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                  298182
```

(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

Seq. ID LIB3150-097-P1-N1-G7

Method BLASTX NCBI GI g1184774 BLAST score 204 E value 8.0e-25 Match length 95 % identity

(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description

GAPC3 [Zea mays]

Seq. No. 298183

Seq. ID LIB3150-097-P1-N1-H10

Method BLASTN



```
NCBI GI
                  q571474
BLAST score
                  33
E value
                  4.0e-09
Match length
                  65
% identity
                  88
                  Chlamydomonas reinhardtii histone H3 (ch3-III), histone H4
NCBI Description
                  (ch4-III), histone H2B (ch2b-III) and histone H2A
                  (ch2a-III) genes, complete cds
Seq. No.
                  298184
                  LIB3150-098-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1658313
BLAST score
                  210
E value
                  6.0e-17
Match length
                  52
% identity
                  75
NCBI Description
                  (Y08987) osr40g2 [Oryza sativa]
Seq. No.
                  298185
Seq. ID
                  LIB3150-098-P1-N1-B9
Method
                  BLASTX
NCBI GI
                  q3176711
BLAST score
                  192
E value
                  1.0e-14
Match length
                  88
% identity
                  57
NCBI Description
                  (AC002392) bZIP-like protein [Arabidopsis thaliana]
Seq. No.
                  298186
Seq. ID
                  LIB3150-098-P1-N1-D3
Method
                  BLASTX
                  g4469005
NCBI GI
BLAST score
                  242
                  2.0e-20
E value
Match length
                  88
% identity
                  51
NCBI Description
                 (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  298187
Seq. ID
                  LIB3150-098-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  q3015621
BLAST score
                  236
                  3.0e-20
E value
Match length
                  72
% identity
                  72
NCBI Description
                  (AF035460) low molecular weight heat shock protein
                  precursor [Zea mays]
                  298188
Seq. No.
Seq. ID
                  LIB3150-098-P1-N1-H4
```

Method BLASTX
NCBI GI g2499932
BLAST score 172
E value 1.0e-12
Match length 52



```
% identity
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi 726305
                  (U22442) adenine phosphoribosyltransferase form 1 [Triticum
                  aestivum]
                  298189
Seq. No.
                  LIB3150-099-P1-N1-F12
Seq. ID
                  BLASTX
Method
                  q3687251
NCBI GI
                  208
BLAST score
E value
                  8.0e-17
Match length
                  62
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
                  298190
Seq. No.
                  LIB3150-099-P1-N1-H8
Seq. ID
Method
                  BLASTN
                  g22172
NCBI GI
                  39
BLAST score
                  1.0e-12
E value
                  71
Match length
                  89
% identity
NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit
                   298191
Seq. No.
                  LIB3150-100-P1-N1-A7
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2811133
                   125
BLAST score
E value
                   4.0e-64
                   201
Match length
% identity
                  Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
NCBI Description
                   partial cds
Seq. No.
                   298192
                   LIB3150-100-P1-N1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4530611
BLAST score
                   401
                   4.0e-39
E value
Match length
                   81
                   91
 % identity
                   (AF134552) serine/threonine protein phosphatase PP2A-2
NCBI Description
                   catalytic subunit [Oryza sativa subsp. indica]
                   298193
 Seq. No.
                   LIB3150-100-P1-N1-E12
 Seq. ID
                   BLASTX
 Method
                   g2244760
 NCBI GI
                   155
 BLAST score
```

(Z97335) selenium-binding protein [Arabidopsis thaliana]

9.0e-11

62

50

E value

Match length

NCBI Description

% identity

BLAST score

Match length

E value

61

207

9.0e-26



```
298194
Seq. No.
                  LIB3150-100-P1-N1-H3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1037129
                  284
BLAST score
                  1.0e-159
E value
                  358
Match length
                  95
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298195
Seq. No.
                  LIB3150-100-P1-N1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1168609
BLAST score
                  188
                   2.0e-14
E value
                  71
Match length
                   51
% identity
                  AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071
NCBI Description
                   auxin-resistance protein AXR1 - Arabidopsis thaliana
                   >gi 304104 (L13922) ubiquitin-activating enzyme E1
                   [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to
                   Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana]
                   >gi_448755_prf__1917\overline{3}37A ubiquitin-activating enzyme E1
                   [Arabidopsis thaliana]
                   298196
Seq. No.
                   LIB3150-100-P2-K1-C5
Seq. ID
                   BLASTX
Method
                   q445612
NCBI GI
                   149
BLAST score
                   2.0e-09
E value
                   39
Match length
                   77
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                   298197
Seq. No.
                   LIB3150-100-P2-K1-D1
Seq. ID
Method
                   BLASTX
                   q1351270
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   53
Match length
% identity
                   89
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
                   5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                   isomerase [Oryza sativa]
Seq. No.
                   298198
                   LIB3150-100-P2-K1-D8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22469
```

NCBI Description

```
% identity
NCBI Description Maize mRNA for cytoplasmic ribosomal protein S11
                  298199
Seq. No.
                  LIB3150-100-P2-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3372518
                  635
BLAST score
E value
                  1.0e-66
                   123
Match length
% identity
NCBI Description (AF050631) invertase [Zea mays]
                   298200
Seq. No.
                  LIB3150-101-P1-N1-C3
Seq. ID
                  BLASTX
Method
                   g1711036
NCBI GI
BLAST score
                   322
                   5.0e-30
E value
                   98
Match length
                   66
% identity
                   (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
NCBI Description
                   sativum]
                   298201
Seq. No.
                   LIB3150-101-P1-N1-F11
Seq. ID
                   BLASTX
Method
                   a1184774
NCBI GI
BLAST score
                   401
                   3.0e-39
E value
                   91
Match length
                   85
% identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   298202
Seq. No.
                   LIB3150-102-P2-K1-E7
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2340107
                   95
BLAST score
                   4.0e-46
E value
                   186
Match length
                   89
% identity
                   Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial
NCBI Description
                   cds
                   298203
Seq. No.
                   LIB3150-103-P2-K1-A11
Seq. ID
                   BLASTX
Method
                   g136063
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
                   35
Match length
                   91
 % identity
```

41868

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_68426_pir__ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate

NCBI Description

```
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009 (D00012)
```

```
triosephosphate isomerase [Zea mays]
                  298204
Seq. No.
                  LIB3150-103-P2-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076531
                  166
BLAST score
                  2.0e-11
E value
                   38
Match length
% identity
                  hypothetical protein, pollen allergen homolog - garden pea
NCBI Description
                   >gi 2129891 pir S65056 pollen allergen homolog precursor
                   (clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)
                   homology with pollen allergens [Pisum sativum]
                   298205
Seq. No.
                   LIB3150-103-P2-K1-D3
Seq. ID
                   BLASTX
Method
                   q4150963
NCBI GI
                   164
BLAST score
                   3.0e-11
E value
                   57
Match length
                   60
% identity
                   (Y18620) DsPTP1 protein [Arabidopsis thaliana]
NCBI Description
                   298206
Seq. No.
                   LIB3150-103-P2-K1-E8
Seq. ID
Method
                   BLASTN
                   q625147
NCBI GI
                   144
BLAST score
                   3.0e-75
E value
                   270
Match length
                   97
% identity
                   Zea mays protein disulfide isomerase (pdi) mRNA, complete
NCBI Description
Seq. No.
                   298207
                   LIB3150-103-P2-K1-F7
Seq. ID
Method
                   BLASTX
                   q1076820
NCBI GI
                   166
BLAST score
                   1.0e-11
E value
                   41
Match length
 % identity
                   phosphoglycerate mutase (EC 5.4.2.1) - maize
NCBI Description
                   298208
 Seq. No.
                   LIB3150-103-P2-K1-G12
 Seq. ID
 Method
                   BLASTX
                   q731827
 NCBI GI
                   143
 BLAST score
                    9.0e-09
 E value
                    54
 Match length
 % identity
                    50
```

MITOCHONDRIAL ACIDIC PROTEIN MAM33 PRECURSOR

>gi_626327_pir__S48409 hypothetical protein YIL070c - yeast



(Saccharomyces cerevisiae) >gi_557799_emb_CAA86153_(Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces cerevisiae]

 Seq. No.
 298209

 Seq. ID
 LIB3150-104-P2-K1-A5

 Method
 BLASTX

 NCBI GI
 q1762945

NCBI GI g1762945 BLAST score 150 E value 1.0e-09 Match length 45 % identity 69

NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana

tabacum]

Seq. No. 298210

Seq. ID LIB3150-104-P2-K1-D5

Method BLASTX
NCBI GI g3790441
BLAST score 148
E value 2.0e-09
Match length 36
% identity 89

NCBI Description (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]

Seq. No. 298211

Seq. ID LIB3150-104-P2-K1-D8

Method BLASTN
NCBI GI g2662309
BLAST score 41
E value 8.0e-14
Match length 61
% identity 92

NCBI Description Hordeum vulgare mRNA for bpw1, complete cds

Seq. No. 298212

Seq. ID LIB3150-104-P2-K1-F1

Method BLASTX
NCBI GI g3334323
BLAST score 374
E value 7.0e-36
Match length 87
% identity 83

NCBI Description GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog

[Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1

(AF001308) SAR1/GTP-binding secretory factor [Arabidopsis

thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis

thaliana]

Seq. No. 298213

Seq. ID LIB3150-104-P2-K1-F2

Method BLASTN
NCBI GI g3925236
BLAST score 74
E value 2.0e-33
Match length 152
% identity 87



```
NCBI Description Zea mays 6-phosphogluconate dehydrogenase gene, partial cds
Seq. No.
                  298214
                  LIB3150-104-P2-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3763917
BLAST score
                  209
E value
                  8.0e-17
Match length
                  44
                  84
% identity
NCBI Description
                  (AC004450) hypothetical protein [Arabidopsis thaliana]
                  >gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224)
                  hypothetical protein [Arabidopsis thaliana]
                  298215
Seq. No.
                  LIB3150-105-P2-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g902526
BLAST score
                  84
E value
                  1.0e-39
Match length
                  136
% identity
                  90
NCBI Description
                  Zea mays clone MubG7 ubiquitin fusion protein gene,
                  complete cds
                  298216
Seq. No.
Seq. ID
                  LIB3150-105-P2-K1-B7
Method
                  BLASTN
NCBI GI
                  g2642323
BLAST score
                  246
E value
                  1.0e-136
                  279
Match length
                  97
% identity
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds
Seq. No.
                  298217
                  LIB3150-105-P2-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g217973
BLAST score
                  131
E value
                  1.0e-67
                  230
```

Match length

92 % identity

NCBI Description Zea mays gene for triosephosphate isomerase, complete cds

298218 Seq. No.

LIB3150-105-P2-K1-G1 Seq. ID

Method BLASTN NCBI GI g602252 BLAST score 42 E value 1.0e-14 Match length 211 % identity 78

NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 298219

Seq. ID LIB3150-106-P2-K1-B5

```
Method
                  BLASTX
                  g2230873
NCBI GI
                  197
BLAST score
                  4.0e-15
E value
Match length
                  67
                  60
% identity
                  (X98494) M phase phosphoprotein 10 [Homo sapiens]
NCBI Description
                  298220
Seq. No.
                  LIB3150-106-P2-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                   q1335965
BLAST score
                   40
                   3.0e-13
E value
                   148
Match length
                   82
% identity
NCBI Description Zea mays acetyl CoA carboxylase mRNA, partial cds
                   298221
Seq. No.
                   LIB3150-106-P2-K1-F3
Seq. ID
Method
                   BLASTX
                   q1172977
NCBI GI
BLAST score
                   359
E value
                   3.0e - 34
                   77
Match length
                   86
% identity
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
                   298222
Seq. No.
                   LIB3150-106-P2-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076800
BLAST score
                   215
                   3.0e-17
E value
                   57
Match length
% identity
                   77
                   L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                   maize >qi 600116 emb CAA84406 (Z34934) cytosolic ascorbate
                   peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
                   peroxidase [Zea mays]
                   298223
Seq. No.
                   LIB3150-106-P2-K1-H3
Seq. ID
Method
                   BLASTN
                   g22144
NCBI GI
BLAST score
                   292
                   1.0e-163
E value
                   344
Match length
                   96
% identity
                   Maize anaerobically regulated gene for fructose
NCBI Description
                   bisphosphate aldolase (EC 4.1.2.13)
                   298224
Seq. No.
                   LIB3150-106-P2-K1-H8
Seq. ID
```

BLASTX

g2996166

Method NCBI GI



```
BLAST score
                   5.0e-22
E value
                   55
Match length
                   82
% identity
                   (AF051757) putative 60S ribosomal protein L15 [Picea
NCBI Description
                   mariana] >gi_2996168 (AF051758) putative 60S ribosomal protein L15 [Picea mariana] >gi_2996170 (AF051759) putative
                   60S ribosomal protein L15 [Picea mariana]
                   298225
Seq. No.
                   LIB3150-107-P1-N1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3548818
                   206
BLAST score
                   3.0e-16
E value
                   113
Match length
                    43
% identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   298226
Seq. No.
                   LIB3150-107-P1-N1-E4
Seq. ID
                   BLASTN
Method
NCBI GI
                   q577818
BLAST score
                    62
                    2.0e-26
E value
                    125
Match length
                    89
% identity
                   Z.mays gene for H2B histone (gH2B4)
NCBI Description
                    298227
Seq. No.
                    LIB3150-107-P1-N1-F4
Seq. ID
                    BLASTX
Method
                    g462195
NCBI GI
BLAST score
                    242
                    2.0e-20
E value
Match length
                    71
% identity
                    66
                    PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi_100682_pir__S21636 GOS2 protein - rice
                    >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                    >gi 3789950 (AF094774) translation initiation factor [Oryza
                    sativa]
                    298228
Seq. No.
                    LIB3150-107-P1-N1-H4
Seq. ID
                    BLASTX
Method
                    g4510423
NCBI GI
                    175
BLAST score
                    7.0e-13
E value
                    87
Match length
                    45
 % identity
```

(AC006929) unknown protein [Arabidopsis thaliana] NCBI Description

298229 Seq. No.

LIB3150-107-P2-K1-A10 Seq. ID

BLASTN Method NCBI GI q498774



```
BLAST score
                  1.0e-120
E value
                  267
Match length
                  96
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein
                  298230
Seq. No.
                  LIB3150-107-P2-K1-B10
Seq. ID
                  BLASTX
Method
                  q2492519
NCBI GI
BLAST score
                  161
                  6.0e-11
E value
Match length
                   43
                   77
% identity
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi 1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
                   298231
Seq. No.
                   LIB3150-107-P2-K1-B5
Seq. ID
                   BLASTN
Method
                   g498772
NCBI GI
BLAST score
                   143
                   1.0e-74
E value
Match length
                   252
                   89
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
                   298232
Seq. No.
                   LIB3150-107-P2-K1-F12
Seq. ID
                   BLASTN
Method
                   g2341060
NCBI GI
BLAST score
                   181
E value
                   3.0e-97
                   285
Match length
% identity
                   91
                   Zea mays translational initiation factor eIF-4A (tif-4A3)
NCBI Description
                   mRNA, complete cds
                   298233
Seq. No.
                   LIB3150-107-P2-K1-H2
Seq. ID
                   BLASTN
Method
                   g22324
NCBI GI
BLAST score
                   172
                   6.0e-92
E value
                   212
Match length
 % identity
                   95
 NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
                   298234
 Seq. No.
                   LIB3150-108-P1-N1-A11
 Seq. ID
                   BLASTX
 Method
                   g1658313
 NCBI GI
                   148
 BLAST score
                   2.0e-09
 E value
                   102
 Match length
```

39

% identity



```
NCBI Description (Y08987) osr40g2 [Oryza sativa]
                  298235
Seq. No.
                  LIB3150-108-P1-N1-C4
Seq. ID
                  BLASTX
Method
                  q419803
NCBI GI
                  347
BLAST score
                  1.0e-32
E value
                  122
Match length
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  298236
Seq. No.
                  LIB3150-108-P1-N1-C5
Seq. ID
                  BLASTX
Method
                  g168664
NCBI GI
                   317
BLAST score
                   2.0e-29
E value
                   65
Match length
                   88
% identity
NCBI Description (M13507) zein protein precursor [Zea mays]
                   298237
Seq. No.
                   LIB3150-108-P1-N1-E2
Seq. ID
                   BLASTX
Method
                   q3335372
NCBI GI
                   172
BLAST score
                   3.0e-12
E value
                   122
Match length
% identity
                  (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
                   298238
Seq. No.
                   LIB3150-108-P1-N1-E5
 Seq. ID
Method
                   BLASTX
                   q1658313
NCBI GI
                   321
 BLAST score
                   8.0e-30
 E value
Match length
                   91
                   34
 % identity
                  (Y08987) osr40g2 [Oryza sativa]
 NCBI Description
                   298239
 Seq. No.
                   LIB3150-108-P1-N1-G2
 Seq. ID
                   BLASTX
 Method
                   g3746936
 NCBI GI
 BLAST score
                   175
 E value
                   3.0e-13
 Match length
                   69
                   54
 % identity
 NCBI Description (AF091808) actin 1 [Anemia phyllitidis]
                   298240
 Seq. No.
                   LIB3150-108-P1-N1-H7
 Seq. ID
                   BLASTX
 Method
```

g2282584

NCBI GI



```
486
BLAST score
                  4.0e-49
E value
                  110
Match length
                  85
% identity
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]
                  298241
Seq. No.
                  LIB3150-108-P2-K1-B9
Seq. ID
                  BLASTN
Method
                   g1575127
NCBI GI
                   103
BLAST score
                   1.0e-50
E value
                   345
Match length
                   82
% identity
NCBI Description Zea mays lumenal binding protein cBiPe2 mRNA, complete cds
                   298242
Seq. No.
                   LIB3150-108-P2-K1-E10
Seq. ID
                   BLASTX
Method
                   g445613
NCBI GI
                   174
BLAST score
                   2.0e-12
E value
                   50
Match length
                   64
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                   298243
Seq. No.
                   LIB3150-108-P2-K1-E5
Seq. ID
                   BLASTN
Method
                   q168512
NCBI GI
                   147
BLAST score
                   6.0e-77
E value
                   365
Match length
                   88
% identity
                   Maize major protein (L3) mRNA from the surface of lipid
NCBI Description
                   bodies, 3' end
                   298244
 Seq. No.
                   LIB3150-108-P2-K1-F7
 Seq. ID
 Method
                   BLASTX
                   g4512699
 NCBI GI
                   181
 BLAST score
                   3.0e-13
 E value
                   53
 Match length
 % identity
                    62
                    (AC006569) putative NADH-ubiquinone oxireductase
 NCBI Description
                    [Arabidopsis thaliana]
                    298245
 Seq. No.
                    LIB3150-108-P2-K1-H3
 Seq. ID
                    BLASTN
 Method
                    q1184773
 NCBI GI
                    154
 BLAST score
                    3.0e-81
 E value
 Match length
                    182
                    97
 % identity
 NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
```

*



(qpc3) mRNA, complete cds

```
298246
Seq. No.
                  LIB3150-109-P2-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827700
BLAST score
                  200
                  2.0e-15
E value
                  84
Match length
                   49
% identity
                   (ALO21684) DEAD box ATP dependent helicase protein
NCBI Description
                   [Arabidopsis thaliana]
                   298247
Seq. No.
Seq. ID
                  LIB3150-109-P2-K1-B5
                  BLASTX
Method
                   q4309698
NCBI GI
BLAST score
                   307
E value
                   4.0e-28
                   130
Match length
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   298248
                   LIB3150-109-P2-K1-D12
Seq. ID
                   BLASTN
Method
                   a22272
NCBI GI
BLAST score
                   98
                   1.0e-47
E value
                   287
Match length
                   86
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.
                   298249
                   LIB3150-109-P2-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q168505
BLAST score
                   41
E value
                   5.0e-14
Match length
                   45
                   98
% identity
NCBI Description Zea mays histone H3 gene, complete cds
                   298250
Seq. No.
                   LIB3150-109-P2-K1-F10
Seq. ID
Method
                   BLASTX
                   g1169533
NCBI GI
                   335
BLAST score
                   3.0e - 31
E value
Match length
                   81
                   85
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
```

41877

frontalis]

>gi_515827_emb_CAA56645_ (X80474) enolase [Neocallimastix



```
Seq. No.
                  298251
                  LIB3150-109-P2-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136057
BLAST score
                  194
E value
                  9.0e-15
Match length
                  45
                  84
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi_556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
                   298252
Seq. No.
                  LIB3150-109-P2-K1-H10
Seq. ID
Method
                  BLASTN
                  q998429
NCBI GI
BLAST score
                   144
                   3.0e-75
E value
                   333
Match length
% identity
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                   5348 nt]
                   298253
Seq. No.
                   LIB3150-110-P2-K1-C4
Seq. ID
                  BLASTN
Method
                   q22272
NCBI GI
BLAST score
                   72
                   3.0e-32
E value
                   215
Match length
                   82
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.
                   298254
                   LIB3150-110-P2-K1-D11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1532072
BLAST score
                   72
                   4.0e-32
E value
Match length
                   247
% identity
                   81
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
                   298255
Seq. No.
Seq. ID
                   LIB3150-110-P2-K1-D12
Method
                   BLASTN
NCBI GI
                   q312178
BLAST score
                   89
                   2.0e-42
E value
                   143
Match length
                   58
% identity
NCBI Description Z.mays GapC2 gene
```

Method BLASTN

298256

LIB3150-110-P2-K1-G2

Seq. No. Seq. ID

```
NCBI GI
                  q531832
BLAST score
                  36
                  3.0e-11
E value
Match length
                  76
                  87
% identity
NCBI Description Cloning vector pSport2, complete sequence
                  298257
Seq. No.
                  LIB3150-110-P2-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q902585
BLAST score
                  35
E value
                  4.0e-10
Match length
                  55
                  91
% identity
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
Seq. No.
                  298258
                  LIB3150-111-P2-K1-C5
Seq. ID
Method
                  BLASTN
                  g293886
NCBI GI
                  38
BLAST score
E value
                  6.0e-12
Match length
                  74
                  88
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
NCBI Description
                  end, (clone GAPC3)
Seq. No.
                  298259
Seq. ID
                  LIB3150-112-P2-K1-A3
Method
                  BLASTX
NCBI GI
                  g2695941
BLAST score
                  200
E value
                  1.0e-15
Match length
                  50
                  76
% identity
NCBI Description (AJ222784) ribosomal like-protein [Hordeum vulgare]
Seq. No.
                  298260
Seq. ID
                  LIB3150-112-P2-K1-A5
Method
                  BLASTX
NCBI GI
                   g2498077
BLAST score
                   510
E value
                  8.0e-52
                   99
Match length
                   97
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
                   298261
Seq. No.
```

Seq. ID LIB3150-112-P2-K1-A6

Method BLASTN
NCBI GI g2431766
BLAST score 173
E value 1.0e-92
Match length 217



```
% identity
                  Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,
NCBI Description
                  complete cds
                  298262
Seq. No.
Seq. ID
                  LIB3150-112-P2-K1-B7
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  392
                  5.0e-38
E value
Match length
                  88
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
                  298263
Seq. No.
Seq. ID
                  LIB3150-112-P2-K1-C2
                  BLASTX
Method
                  q19614
NCBI GI
                  171
BLAST score
E value
                  4.0e-12
Match length
                   45
% identity
                  78
                  (X13677) histone H3 (AA 1-58) [Medicago sativa]
NCBI Description
                   298264
Seq. No.
Seq. ID
                  LIB3150-112-P2-K1-F5
Method
                   BLASTN
                   q1184773
NCBI GI
                   44
BLAST score
                   9.0e-16
E value
                   116
Match length
% identity
                   86
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
NCBI Description
                   (gpc3) mRNA, complete cds
                   298265
Seq. No.
                   LIB3150-112-P2-K1-G3
Seq. ID
Method
                   BLASTX
                   q1653293
NCBI GI
BLAST score
                   160
                   8.0e-11
E value
Match length
                   58
% identity
                   57
                  (D90912) ornithine acetyltransferase [Synechocystis sp.]
NCBI Description
                   298266
Seq. No.
                   LIB3150-112-P2-K1-H5
Seq. ID
                   BLASTN
Method
                   g2257755
NCBI GI
BLAST score
                   202
                   1.0e-110
E value
                   311
Match length
                   91
% identity
                   Zea mays nucleolar histone deacetylase HD2-p39 mRNA,
NCBI Description
```

complete cds

Seq. ID

```
298267
Seq. No.
                  LIB3150-113-P2-K1-C5
Seq. ID
                  BLASTN
Method
                  g2345153
NCBI GI
BLAST score
                  175
                  8.0e-94
E value
                  255
Match length
                  93
% identity
NCBI Description Zea mays ribsomal protein S4 (rps4) mRNA, complete cds
Seq. No.
                  298268
                  LIB3150-113-P2-K1-C6
Seq. ID
Method
                  BLASTN
                  q3294466
NCBI GI
                  43
BLAST score
                  4.0e-15
E value
Match length
                  127
                  82
% identity
NCBI Description Zea mays phosphoglucomutase 1 mRNA, complete cds
                  298269
Seq. No.
Seq. ID
                  LIB3150-113-P2-K1-G5
Method
                  BLASTN
                  q22516
NCBI GI
                  160
BLAST score
                  6.0e-85
E value
                  212
Match length
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                  298270
Seq. No.
                  LIB3150-113-P2-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581156
BLAST score
                  290
                   5.0e-26
E value
                  63
Match length
% identity
                   90
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
                   298271
Seq. No.
                   LIB3150-114-P2-K1-C8
Seq. ID
Method
                  BLASTX
                   g1174536
NCBI GI
                   144
BLAST score
                   5.0e-09
E value
                   37
Match length
                   70
% identity
                  ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE--TRNA LIGASE)
NCBI Description
                   (ASNRS) >gi 1073865 pir B64115 asparagine--tRNA ligase (EC
                   6.1.1.22) - Haemophilus influenzae (strain Rd KW20)
                   >gi 1574761 (U32810) asparaginyl-tRNA synthetase (asnS)
                   [Haemophilus influenzae Rd]
                   298272
Seq. No.
```

41881

LIB3150-114-P2-K1-H5

NCBI GI

q998429



```
BLASTN
Method
NCBI GI
                  q168694
                  59
BLAST score
E value
                  1.0e-24
Match length
                  125
                  94
% identity
NCBI Description Maize gamma zein mRNA, partial cds
                  298273
Seq. No.
                  LIB3150-116-P2-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706323
BLAST score
                  217
                  2.0e-17
E value
Match length
                  114
                  45
% identity
                  ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704
NCBI Description
                  ornithine decarboxylase (EC 4.1.1.17) - jimsonweed
                  >gi 871008_emb_CAA61121_ (X87847) ornithine decarboxylase
                   [Datura stramonium]
                  298274
Seq. No.
                  LIB3150-116-P2-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1895083
BLAST score
                   34
                  1.0e-09
E value
                  86
Match length
                   85
% identity
                  Zea mays golgi associated protein se-wap41 mRNA, complete
NCBI Description
Seq. No.
                   298275
Seq. ID
                   LIB3150-117-P2-K1-B7
Method
                   BLASTX
NCBI GI
                   q2642446
BLAST score
                   154
                   3.0e-10
E value
Match length
                   51
% identity
                   65
                   (ACO02391) similar to auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   298276
                   LIB3150-117-P2-K1-F8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2104711
BLAST score
                   41
                   6.0e-14
E value
Match length
                   69
                   90
% identity
NCBI Description Zea mays endosperm specific protein mRNA, complete cds
Seq. No.
                   298277
                   LIB3150-117-P2-K1-G4
Seq. ID
                   BLASTN
Method
```

``



```
a
BLAST score
    E value
                              1.0e-115
                              319
    Match length
    % identity
                              91
                              GRF1=general regulatory factor [Zea mays, XL80, Genomic,
    NCBI Description
                              298278
    Seq. No.
                              LIB3150-117-P2-K1-H6
    Seq. ID
    Method
                              BLASTX
    NCBI GI
                              q4506635
    BLAST score
                              186
    E value
                              5.0e-14
    Match length
                              61
    % identity
                             ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S
RIBOSOMAL PROTEIN L32 >gi_71335_pir__R5HU32_ribosomal
protein L32 - human >gi_71336_pir__R5MS32_ribosomal protein
L32 - mouse >gi_71337_pir__R5RT32_ribosomal protein L32 -
rat >gi_36132_emb_CAA27048_(X03342)_rpL32_(aa 1-135)_[Homo
sapiens] >gi_57117_emb_CAA29777_(X06483)_ribosomal_protein
L32_[Rattus_norvegicus] >gi_200781_(K02060)_ribosomal_protein_L32_37_[Mus_musculus] >gi_226004_prf__14053397_
    NCBI Description
                              protein L32-3A [Mus musculus] >gi_226004_prf__1405339A
                              ribosomal protein L32 [Rattus norvegicus]
    Seq. No.
                              298279
                              LIB3150-118-P2-K1-G9
    Seq. ID
    Method
                              BLASTN
    NCBI GI
                              g2431770
                              60
    BLAST score
                              5.0e-25
    E value
                              228
    Match length
     % identity
                              82
                              Zea mays acidic ribosomal protein P2b (rpp2b) mRNA,
    NCBI Description
                              complete cds
     Seq. No.
                              298280
     Seq. ID
                              LIB3151-001-P1-K1-A11
     Method
                              BLASTX
     NCBI GI
                              q22216
     BLAST score
                              246
                              4.0e-21
     E value
                              64
     Match length
                              80
     % identity
     NCBI Description
                              (X55722) 22kD zein [Zea mays]
                              298281
     Seq. No.
     Seq. ID
                              LIB3151-001-P1-K1-A4
     Method
                              BLASTX
     NCBI GI
                              q121472
                              144
     BLAST score
                              3.0e-12
     E value
                              88
     Match length
                              50
     % identity
                              GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
     NCBI Description
```

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -



maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

 Seq. No.
 298282

 Seq. ID
 LIB3151-001-P1-K1-A8

 Method
 BLASTX

 NCBI GI
 g141597

 BLAST score
 346

BLAST score 346 E value 1.0e-32 Match length 129 % identity 63

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 298283

Seq. ID LIB3151-001-P1-K1-B6

Method BLASTX
NCBI GI g168701
BLAST score 520
E value 8.0e-55
Match length 140
% identity 79

NCBI Description (M60837) zein [Zea mays]

Seq. No. 298284

Seq. ID LIB3151-001-P1-K1-B7

Method BLASTN
NCBI GI g22549
BLAST score 227
E value 1.0e-125
Match length 311
% identity 93

NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298285

Seq. ID LIB3151-001-P1-K1-C12

Method BLASTX
NCBI GI g141608
BLAST score 160
E value 2.0e-11
Match length 64
% identity 62

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655

zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa

zein [Zea mays]

Seq. No. 298286

Seq. ID LIB3151-001-P1-K1-C5

Method BLASTX
NCBI GI g141597
BLAST score 311
E value 2.0e-28
Match length 116
% identity 60

```
ZEIN-ALPHA PRECURSOR (19 KD) (CLO
```

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) NCBI Description >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays] 298287 Seq. No. Seq. ID LIB3151-001-P1-K1-D10 Method BLASTX q141617 NCBI GI 243 BLAST score E value 2.0e-21 Match length 101 % identity ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) NCBI Description >gi_100941_pir__S12140 zein Zc1 - maize >gi_100945_pir__B29017 zein 2 - maize >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays] >gi 168666 (M16460) 16-kDa zein protein [Zea mays] 298288 Seq. No. LIB3151-001-P1-K1-D12 Seq. ID BLASTN Method NCBI GI q168484 BLAST score 279 1.0e-156 E value 355 Match length 95 % identity NCBI Description Maize endosperm glutelin-2 gene, complete cds 298289 Seq. No. LIB3151-001-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g224513 BLAST score 172 E value 7.0e-13 Match length 51 75 % identity NCBI Description zein M6 [Zea mays] 298290 Seq. No. LIB3151-001-P1-K1-D8 Seq. ID BLASTX Method g135060 NCBI GI BLAST score 405 1.0e-39 E value 90 Match length % identity 87 SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) NCBI Description (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_ $\overline{2}248\overline{6}$ emb_CAA26247_ (X02400) sucrose synthase [Zea mays] $>gi_22488_{emb}$ CAA26229_ (X02382) sucrose synthase [Zea mays]

Seq. No. 298291

Seq. ID LIB3151-001-P1-K1-E12

Method BLASTN NCBI GI g4185305



```
BLAST score
 E value
                    1.0e-104
                    289
 Match length
                    92
 % identity
                    Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
 NCBI Description
                    (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                    protein, polyprotein, and copia protein genes, complete
                    cds; and unknown genes
                    298292
 Seq. No.
                    LIB3151-001-P1-K1-E4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1172977
                    217
 BLAST score
                    1.0e-17
 E value
                    92
 Match length
                    50
 % identity
                    60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
 NCBI Description
                    ribosomal protein L18 [Arabidopsis thaliana]
                    298293
 Seq. No.
                    LIB3151-001-P1-K1-E7
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2832243
 BLAST score
                    180
  E value
                    2.0e-13
                    74
 Match length
                    55
  % identity
  NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                    298294
  Seq. No.
                    LIB3151-001-P1-K1-F2
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    g22549
                    238
  BLAST score
  E value
                    1.0e-131
Match length
                    278
                    97
  % identity
  NCBI Description Maize gene for a 27kDa storage protein, zein
                     298295
  Seq. No.
                     LIB3151-001-P1-K1-F4
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                     g168695
                     157
  BLAST score
                     2.0e-10
  E value
  Match length
                     89
                     46
  % identity
                     (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
  NCBI Description
                     zein gamma [Zea mays]
                     298296
  Seq. No.
                     LIB3151-001-P1-K1-F7
  Seq. ID
                     BLASTN
  Method
                     g168681
  NCBI GI
```

102

4.0e-50

BLAST score

E value



```
Match length
% identity
                  86
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi 270686_gb_I03333_ Sequence 8 from Patent US
                  298297
Seq. No.
                  LIB3151-001-P1-K1-G10
Seq. ID
Method
                  BLASTN
                  g22549
NCBI GI
                  33
BLAST score
                   3.0e-09
E value
Match length
                   61
% identity
                   89
NCBI Description Maize gene for a 27kDa storage protein, zein
                   298298
Seq. No.
                   LIB3151-001-P1-K1-G11
Seq. ID
Method
                   BLASTX
                   g22122
NCBI GI
                   222
BLAST score
                   2.0e-18
E value
                   53
Match length
                   87
% identity
                   (X04050) alcohol dehydrogenase 1 [Zea mays] >gi_3420021
NCBI Description
                   (AF050457) alcohol dehydrogenase 1 [Zea mays]
                   298299
Seq. No.
                   LIB3151-001-P1-K1-H11
Seq. ID
Method
                   BLASTN
                   g22549
NCBI GI
                   113
BLAST score
                   6.0e-57
E value
Match length
                   197
% identity
                   89
NCBI Description Maize gene for a 27kDa storage protein, zein
                   298300
Seq. No.
                   LIB3151-001-P1-K1-H8
Seq. ID
                   BLASTN
Method
                   g168665
NCBI GI
                   208
BLAST score
                   1.0e-113
E value
                   252
Match length
                   96
 % identity
 NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                   298301
 Seq. No.
                   LIB3151-002-P1-K1-A3
 Seq. ID
                   BLASTX
 Method
```

Method BLASTX
NCBI GI g121472
BLAST score 142
E value 7.0e-09
Match length 70
% identity 44

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -

maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

 Seq. No.
 298302

 Seq. ID
 LIB3151-002-P1-K1-A7

 Method
 BLASTX

 MCDI GI
 CP3660

NCBI GI g82660
BLAST score 162
E value 3.0e-11
Match length 62
% identity 56

NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment) >gi 809117 emb CAA24720 (V01473) zein [Zea mays]

Seq. No. 298303

Seq. ID LIB3151-002-P1-K1-C2

Method BLASTX
NCBI GI g121472
BLAST score 149
E value 7.0e-22
Match length 106
% identity 54

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea

mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298304

Seq. ID LIB3151-002-P1-K1-C3

Method BLASTX
NCBI GI g135417
BLAST score 209
E value 7.0e-17
Match length 49
% identity 78

NCBI Description TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150 emb_CAA44861_ (X63176)

Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No. 298305

Seq. ID LIB3151-002-P1-K1-C5

Method BLASTX
NCBI GI g550542
BLAST score 183
E value 3.0e-26
Match length 133
% identity 51

NCBI Description (X81831) cytochrome P450 [Zea mays]

>gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea

mays]

Seq. No. 298306

Seq. ID LIB3151-002-P1-K1-C6



```
BLASTX
Method
                   g121472
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
                   110
Match length
                   45
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326 pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                   mays] > \overline{gi}_{168485} (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                   298307
Seq. No.
                   LIB3151-002-P1-K1-D1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g168679
BLAST score
                   40
                   4.0e-13
E value
Match length
                   56
                   93
% identity
                   Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
NCBI Description
                   >gi_270687_gb_I03334_ Sequence 9 from Patent US
                   298308
Seq. No.
                   LIB3151-002-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832246
BLAST score
                   367
E value
                   4.0e-35
Match length
                   124
% identity
                   66
                   (AF031569) 22-kDa alpha zein 8 [Zea mays]
NCBI Description
                   298309
Seq. No.
                   LIB3151-002-P1-K1-E3
Seq. ID
                   BLASTX
Method
                   g121472
NCBI GI
                   184
BLAST score
                   1.0e-13
E value
                   80
Match length
                   49
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517 emb_CAA37594 (X53514) zein Zc2 [Zea
                   mays] >gi 1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
                   298310
Seq. No.
                   LIB3151-002-P1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g16073
BLAST score
                   369
                   2.0e-35
E value
```

109

70

Match length % identity

NCBI GI



```
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  298311
Seq. No.
                  LIB3151-002-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22215
BLAST score
                  70
                  4.0e-31
E value
Match length
                  312
                  84
% identity
NCBI Description Z.mays ZSF4C1 gene for zein
Seq. No.
                  298312
                  LIB3151-002-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2146739
BLAST score
                  227
                  1.0e-18
E value
Match length
                  69
                  65
% identity
NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.
                   298313
                  LIB3151-002-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168699
BLAST score
                   236
                   7.0e-20
E value
Match length
                   68
% identity
                   74
NCBI Description (M60836) zein [Zea mays]
                   298314
Seq. No.
                   LIB3151-002-P1-K1-H2
Seq. ID
                   BLASTX
Method
                   q168701
NCBI GI
                   276
BLAST score
                   1.0e-24
E value
                   96
Match length
                   65
% identity
NCBI Description (M60837) zein [Zea mays]
                   298315
Seq. No.
                   LIB3151-002-P1-K1-H7
Seq. ID
                   BLASTN
Method
                   g168425
NCBI GI
BLAST score
                   180
                   9.0e-97
E value
                   252
Match length
                   93
% identity
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                   298316
Seq. No.
Seq. ID
                   LIB3151-003-Q1-K1-A10
                   BLASTX
Method
```

41890

g2832247

```
261
BLAST score
                  9.0e-23
E value
                  99
Match length
                  58
% identity
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
                  298317
Seq. No.
                  LIB3151-003-Q1-K1-A11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22514
                  33
BLAST score
                  4.0e-09
E value
                  168
Match length
                  80
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.
                  298318
                  LIB3151-003-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141615
BLAST score
                  162
E value
                  2.0e-14
Match length
                  73
                  73
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
NCBI Description
                  >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
                   298319
Seq. No.
                  LIB3151-003-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                   g2440160
NCBI GI
                   215
BLAST score
                   1.0e-17
E value
                   67
Match length
% identity
                   (Y14836) beta-galactosidase [Phagemid cloning vector
NCBI Description
                   pTZ19U]
                   298320
Seq. No.
                   LIB3151-003-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   g121472
NCBI GI
                   205
BLAST score
                   4.0e-16
E value
Match length
                   98
                   45
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb_CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >qi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                   mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
```

Seq. No. 298321

Seq. ID LIB3151-003-Q1-K1-B12

Method BLASTX NCBI GI g548852



```
BLAST score
                  353
                  2.0e-33
E value
                  82
Match length
                  78
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi 303839_dbj_BAA02158_ (D12633) 40S
                   subunit ribosomal protein [Oryza sativa]
                   298322
Seq. No.
                   LIB3151-003-Q1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168484
BLAST score
                   45
                   2.0e-16
E value
                   53
Match length
                   96
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298323
Seq. No.
                   LIB3151-003-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   q4249662
NCBI GI
BLAST score
                   168
E value
                   7.0e-12
Match length
                   87
                   45
% identity
                   (AF089810) Altered Response to Gravity [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   298324
                   LIB3151-003-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g141597
NCBI GI
BLAST score
                   214
                   2.0e-17
E value
Match length
                   108
% identity
                   44
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >qi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   298325
Seq. No.
                   LIB3151-003-Q1-K1-C6
Seq. ID
Method
                   BLASTX
                   q168699
NCBI GI
 BLAST score
                   402
                   3.0e-39
 E value
                   96
Match length
 % identity
                   83
                   (M60836) zein [Zea mays]
 NCBI Description
                   298326
 Seq. No.
                   LIB3151-003-Q1-K1-D1
 Seq. ID
```

BLASTX

g100925

219

Method

NCBI GI BLAST score

BLAST score

Match length

E value

3.0e-15

83

```
6.0e-18
E value
Match length
                  84
% identity
                  zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
NCBI Description
                  (X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.
                  LIB3151-003-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g2982322
NCBI GI
BLAST score
                  246
                  2.0e-21
E value
Match length
                  66
                  74
% identity
                  (AF051246) probable proteasome subunit [Picea mariana]
NCBI Description
                  298328
Seq. No.
                  LIB3151-003-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  q133867
NCBI GI
                   464
BLAST score
                   2.0e-46
E value
                   111
Match length
% identity
                   77
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi 22470_emb_CAA39438_ (X55967)
                   ribosomal protein S11 [Zea mays]
Seq. No.
                   298329
                   LIB3151-003-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   g224508
NCBI GI
                   264
BLAST score
E value
                   5.0e-23
                   82
Match length
% identity
                   68
NCBI Description zein A20 [Zea mays]
                   298330
Seq. No.
                   LIB3151-003-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g133867
BLAST score
                   494
E value
                   5.0e-50
Match length
                   114
                   83
% identity
                   40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                   ribosomal protein S11 [Zea mays]
                   298331
Seq. No.
                   LIB3151-003-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g729737
NCBI GI
                   195
```



```
% identity
                  HMG1/2-LIKE PROTEIN >gi_541981_pir__S39556 HMG protein -
NCBI Description
                  fava bean
                  298332
Seq. No.
Seq. ID
                  LIB3151-003-Q1-K1-E6
Method
                  BLASTX
                  q141605
NCBI GI
                  364
BLAST score
                  6.0e-35
E value
                  93
Match length
                  83
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  298333
Seq. No.
                  LIB3151-003-Q1-K1-F12
Seq. ID
Method
                  BLASTX
                  q4586031
NCBI GI
                  280
BLAST score
                  6.0e-25
E value
                  64
Match length
                  83
% identity
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]
                  298334
Seq. No.
                  LIB3151-003-Q1-K1-F5
Seq. ID
Method
                  BLASTN
                  g168484
NCBI GI
                   285
BLAST score
E value
                  1.0e-159
Match length
                   373
                   95
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298335
Seq. No.
                   LIB3151-003-Q1-K1-G4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22326
BLAST score
                   35
                   3.0e-10
E value
                   82
Match length
                   87
% identity
NCBI Description Z.mays gene for Hageman factor inhibitor
                   298336
Seq. No.
                   LIB3151-003-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g168699
NCBI GI
BLAST score
                   169
```

3.0e-12 E value 82 Match length 51 % identity

(M60836) zein [Zea mays] NCBI Description

298337 Seq. No.

BLAST score

```
LIB3151-003-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3757519
                  383
BLAST score
                  6.0e-37
E value
                  143
Match length
% identity
                  (AC005167) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  298338
Seq. No.
                  LIB3151-003-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                   g3292831
NCBI GI
                   348
BLAST score
                   4.0e-33
E value
Match length
                   104
% identity
                   (AL031018) putative serine/threonine kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   298339
                   LIB3151-003-Q1-K1-H5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22528
BLAST score
                   125
E value
                   6.0e-64
                   347
Match length
                   85
% identity
NCBI Description Zea mays mRNA encoding a zein (clone A20)
                   298340
Seq. No.
                   LIB3151-004-Q1-K1-A11
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4140643
                   46
BLAST score
E value
                   8.0e-17
Match length
                   57
                   95
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
Seq. No.
                   298341
                   LIB3151-004-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g100925
BLAST score
                   178
                   4.0e-13
E value
Match length
                   54
% identity
                   61
                   zein, 27K - maize (fragment) >gi 22550 emb_CAA41175_
NCBI Description
                   (X58197) 27kDa storage protein, zein [Zea mays]
                   298342
Seq. No.
Seq. ID
                   LIB3151-004-Q1-K1-B12
Method
                   BLASTX
                   g121472
NCBI GI
                   222
```

```
4.0e-18
E value
Match length
% identity
                    47
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi_22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517 emb_CAA37594 (X53514) zein Zc2 [Zea
                    mays] >gi_168485 (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                    298343
Seq. No.
                    LIB3151-004-Q1-K1-C11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q141605
BLAST score
                    445
                    2.0e-44
E value
                    100
Match length
                    92
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                    >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                    maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                    298344
Seq. No.
                    LIB3151-004-Q1-K1-C5
Seq. ID
Method
                    BLASTX
                    g2340108
NCBI GI
BLAST score
                    327
                    2.0e-30
E value
                    109
Match length
                    60
% identity
                    (U65948) starch branching enzyme IIa [Zea mays]
NCBI Description
                    298345
Seq. No.
                    LIB3151-004-Q1-K1-C8
Seq. ID
Method
                    BLASTX
                    q3157932
NCBI GI
BLAST score
                    161
                    2.0e-11
E value
                    78
Match length
% identity
                    45
                    (AC002131) Similar to hypothetical protein HYP1 gb_Z97338
NCBI Description
                    from A. thaliana. [Arabidopsis thaliana]
                    298346
Seq. No.
Seq. ID
                    LIB3151-004-Q1-K1-D9
                    BLASTX
Method
                    q141617
NCBI GI
                     259
BLAST score
E value
                     2.0e-22
                     64
Match length
% identity
                     77
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
```

>gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
>gi 168666 (M16460) 16-kDa zein protein [Zea mays]



```
298347
Seq. No.
                  LIB3151-004-Q1-K1-E11
Seq. ID
                  BLASTN
Method
                  g22445
NCBI GI
                  69
BLAST score
E value
                  2.0e-30
Match length
                  137
                  89
% identity
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein
                  298348
Seq. No.
                  LIB3151-004-Q1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1037129
                  98
BLAST score
                  1.0e-47
E value
Match length
                   341
                   83
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298349
Seq. No.
Seq. ID
                   LIB3151-004-Q1-K1-E3
Method
                   BLASTN
                   q535019
NCBI GI
                   119
BLAST score
                   3.0e-60
E value
                   257
Match length
% identity
                   45
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
                   298350
Seq. No.
                   LIB3151-004-Q1-K1-E4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22524
                   107
BLAST score
                   4.0e-53
E value
                   163
Match length
                   91
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                   298351
Seq. No.
                   LIB3151-004-Q1-K1-E6
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                   84
BLAST score
                   2.0e-39
E value
                   128
Match length
                   91
 % identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298352
 Seq. No.
                   LIB3151-004-Q1-K1-F10
 Seq. ID
                   BLASTX
Method
                   q168691
NCBI GI
 BLAST score
                   271
```

6.0e-24

E value



```
Match length
                   61
% identity
                   (M29628) zein [Zea mays]
NCBI Description
                   298353
Seq. No.
                   LIB3151-004-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   q141598
NCBI GI
                   170
BLAST score
                   4.0e-12
E value
                    44
Match length
                    75
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                   >gi_72313_pir__ZIZM99 19K zein precursor (clone ZG99) - maize >gi_22519 emb CAA24717 (V01470) zein [Zea mays]
                   >gi_22534_emb_C\overline{A}A24\overline{7}26_ (V01\overline{4}79) zein [Zea mays]
                    298354
Seq. No.
                    LIB3151-004-Q1-K1-F3
Seq. ID
                    BLASTN
Method
                    q168484
NCBI GI
                    161
BLAST score
                    2.0e-85
E value
                    348
Match length
% identity
                    87
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                    298355
Seq. No.
                    LIB3151-004-Q1-K1-F9
Seq. ID
                    BLASTX
Method
                    g141603
NCBI GI
                    550
BLAST score
                    1.0e-56
E value
                    135
Match length
                    87
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                    >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                    >gi 22529_emb_CAA24723_ (V01476) zein [Zea mays]
 Seq. No.
                    298356
                    LIB3151-004-Q1-K1-G6
 Seq. ID
                    BLASTN
 Method
                    g4336204
 NCBI GI
                    38
 BLAST score
                     5.0e-12
 E value
                     46
 Match length
                     96
 % identity
 NCBI Description Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds
                     298357
 Seq. No.
                     LIB3151-004-Q1-K1-H2
 Seq. ID
                     BLASTX
 Method
                     q1345838
 NCBI GI
                     236
 BLAST score
```

7.0e-20

58

76

E value

Match length

% identity



```
PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
NCBI Description
                  >gi_2130143_pir__S65060 phytoene desaturase precursor -
                  maize >gi_1051180 (U37285) phytoene desaturase [Zea mays]
                  298358
Seq. No.
                  LIB3151-004-Q1-K1-H6
Seq. ID
Method
                  BLASTX
                  g141600
NCBI GI
                  167
BLAST score
                  3.0e-16
E value
Match length
                  98
                  54
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.
                  LIB3151-004-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   g119748
NCBI GI
BLAST score
                   219
                   5.0e-18
E value
                   48
Match length
% identity
                   83
                   FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11),
                   cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690)
                   fructose-bisphosphatase [Spinacia oleracea]
                   298360
Seq. No.
                   LIB3151-005-Q1-K1-A4
Séq. ID
                   BLASTN
Method
NCBI GI
                   q168484
                   280
BLAST score
                   1.0e-156
E value
Match length
                   328
                   96
% identity
                   Maize endosperm glutelin-2 gene, complete cds
NCBI Description
                   298361
Seq. No.
                   LIB3151-005-Q1-K1-B1
Seq. ID
                   BLASTX
Method
                   g419803
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
Match length
                   83
                   52
 % identity
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
 NCBI Description
                   mays]
                   298362
 Seq. No.
 Seq. ID
                   LIB3151-005-Q1-K1-C7
                   BLASTX
 Method
                   g629861
 NCBI GI
```

267

2.0e-23

BLAST score

E value



```
Match length
% identity
                    51
                   zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                    zein Zd1 (19 kDa zein) [Zea mays]
                    298363
Seq. No.
                   LIB3151-005-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                    q266398
NCBI GI
                    349
BLAST score
                    4.0e-33
E value
                    96
Match length
                    68
% identity
                    TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                    INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
                    (X54064) corn Hageman factor inhibitor [Zea mays]
                    298364
Seq. No.
                    LIB3151-005-Q1-K1-E5
Seq. ID
                    BLASTX
Method
NCBI GI
                    g141608
BLAST score
                    316
E value
                    3.0e-29
Match length
                    118
                    60
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir_S15655
NCBI Description
                    zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82) \overline{1}9 kDa
                    zein [Zea mays]
                    298365
Seq. No.
                    LIB3151-005-Q1-K1-E8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q168701
                    169
BLAST score
E value
                    5.0e-12
Match length
                    53
% identity
                    58
                    (M60837) zein [Zea mays]
NCBI Description
                    298366
Seq. No.
                    LIB3151-005-Q1-K1-E9
Seq. ID
                    BLASTX
Method
                    g719291
NCBI GI
BLAST score
                    197
                    2.0e-15
E value
                    83
Match length
                    46
 % identity
                    (U19134) unknown [Arabidopsis thaliana]
NCBI Description
                    >gi 1095007_prf __2107236A SABRE gene [Arabidopsis thaliana]
                    298367
 Seq. No.
                    LIB3151-005-Q1-K1-F1
 Seq. ID
                    BLASTN
 Method
```

g1037129

0.0e+00

349

NCBI GI

E value

BLAST score

Seq. ID

NCBI GI

Method



```
445
Match length
                   95
% identity
                   (gamma-zeinA) = opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298368
Seq. No.
                   LIB3151-005-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                   g168699
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
Match length
                   108
% identity
                   67
                   (M60836) zein [Zea mays]
NCBI Description
                   298369
Seq. No.
                   LIB3151-005-Q1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q121472
                   228
BLAST score
                   5.0e-19
E value
Match length
                   88
% identity
                   49
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >qi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                   mays] >gi_1684\overline{8}5 (M1\overline{6}066\overline{)} glutelin-2 [Zea mays]
                   298370
Seq. No.
                   LIB3151-005-Q1-K1-G11
Seq. ID
Method
                   BLASTN
                   g168665
NCBI GI
                   46
BLAST score
                   5.0e-17
E value
                   217
Match length
                   81
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                   298371
Seq. No.
Seq. ID
                   LIB3151-005-Q1-K1-G4
                   BLASTX
Method
                   g584706
NCBI GI
BLAST score
                   384
                   2.0e-37
E value
                   97
Match length
                   77
% identity
                   ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                   >gi 2130066 pir JC5124 aspartate transaminase (EC
                   2.6.1.1), cytoplasmic - rice >gi 287298 dbj BAA03504
                   (D14673) aspartate aminotransferase [Oryza sativa]
                   298372
Seq. No.
```

41901

LIB3151-005-Q1-K1-G5

BLASTX

q72307

Seq. ID Method

298377

BLASTX

LIB3151-006-Q1-K1-C9

```
BLAST score
                  351
                  2.0e-33
E value
                  112
Match length
                  67
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                  (J01246) 26.99 kd zein protein [Zea mays]
                  298373
Seq. No.
Seq. ID
                  LIB3151-005-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  g141597
                  221
BLAST score
                  1.0e-32
E value
                  130
Match length
                   62
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   298374
Seq. No.
                  LIB3151-006-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                   g141610
NCBI GI
                   184
BLAST score
                   1.0e-13
E value
                   51
Match length
                   75
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                   298375
Seq. No.
Seq. ID
                   LIB3151-006-Q1-K1-C3
Method
                   BLASTX
                   q168664
NCBI GI
BLAST score
                   282
E value
                   2.0e-25
Match length
                   94
                   60
% identity
                   (M13507) zein protein precursor [Zea mays]
NCBI Description
                   298376
Seq. No.
Seq. ID
                   LIB3151-006-Q1-K1-C6
                   BLASTX
Method
                   q141617
NCBI GI
                   271
BLAST score
                   8.0e-24
E value
Match length
                   66
                   77
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi 100941 pir S12140 zein Zc1 - maize
                   >gi_100945_pir__B29017 zein 2 - maize
                   >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
```

```
NCBI GI
                  q2623248
BLAST score
                  471
                  3.0e-47
E value
Match length
                  145
% identity
NCBI Description (AF030882) SU1 isoamylase [Zea mays]
                  298378
Seq. No.
                  LIB3151-006-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4185308
BLAST score
                  175
E value
                   9.0e-13
                   93
Match length
% identity
                   46
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                   298379
Seq. No.
                  LIB3151-006-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                   g629861
NCBI GI
                   233
BLAST score
E value
                   2.0e-19
Match length
                   110
% identity
                   zein Zd1, 19K - maize >gi_535020 emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   298380
                   LIB3151-006-Q1-K1-E8
Seq. ID
                   BLASTN
Method
                   g168425
NCBI GI
BLAST score
                   40
                   2.0e-13
E value
Match length
                   192
% identity
                   81
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
Seq. No.
                   298381
                   LIB3151-006-Q1-K1-F1
Seq. ID
                   BLASTN
Method
                   g22514
NCBI GI
                   156
BLAST score
                   2.0e-82
E value
                   312
Match length
                   88
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   298382
Seq. No.
Seq. ID
                   LIB3151-006-Q1-K1-F4
                   BLASTX
Method
                   g2345154
NCBI GI
BLAST score
                   279
                   6.0e-31
E value
                   94
Match length
                   81
% identity
NCBI Description (AF015522) ribsomal protein S4 [Zea mays]
```

Seq. ID

```
Seq. No.
                  298383
                  LIB3151-006-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g168701
NCBI GI
                  197
BLAST score
                  2.0e-15
E value
                  73
Match length
% identity
NCBI Description (M60837) zein [Zea mays] **
                  298384
Seq. No.
                  LIB3151-006-Q1-K1-H12
Seq. ID
                  BLASTX
Method
                  q22220
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
Match length
                  76
                  49
% identity
NCBI Description (X55723) 22 kD zein [Zea mays]
                  298385
Seq. No.
                  LIB3151-006-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g141608
NCBI GI
                  294
BLAST score
                   2.0e-30
E value
                   113
Match length
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943 pir__S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
                   298386
Seq. No.
                   LIB3151-006-Q1-K1-H8
Seq. ID
Method
                   BLASTX
                   g141615
NCBI GI
                   273
BLAST score
                   2.0e-25
E value
                   89
Match length
                   78
% identity
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
NCBI Description
                   >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
                   298387
Seq. No.
                   LIB3151-007-Q1-K1-A12
Seq. ID
Method
                   BLASTN
                   g1037129
NCBI GI
BLAST score
                   314
                   1.0e-176
E value
                   376
Match length
                   96
% identity
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298388
Seq. No.
```

41904

LIB3151-007-Q1-K1-A2

```
Method
                   BLASTX
NCBI GI
                   g168699
BLAST score
                   566
                   2.0e-58
E value
Match length
                   142
% identity
                   57
NCBI Description
                   (M60836) zein [Zea mays]
                   298389
Seq. No.
Seq. ID
                   LIB3151-007-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   q121472
BLAST score
                    384
                    5.0e-37
E value
                    142
Match length
                    54
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi 72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289 emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                   mays] >gi 1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
Seq. No.
                    298390
Seq. ID
                    LIB3151-007-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                    g141599
BLAST score
                    367
E value
                    4.0e-35
Match length
                    101
% identity
                    75
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                    >gi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) -
                    maize (fragment) >gi_168670 (M12142) 19 kDa zein protein
                    [Zea mays]
                    298391
Seq. No.
                    LIB3151-007-Q1-K1-B9
Seq. ID
Method
                    BLASTX
                    g141603
NCBI GI
BLAST score
                    420
                    2.0e-41
E value
                    104
Match length
% identity
                    87
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                    >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                    >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                    298392
Seq. ID
                    LIB3151-007-Q1-K1-C10
Method
                    BLASTX
NCBI GI
                    g3549665
BLAST score
                    140
                    9.0e-09
E value
                    74
Match length
                    50
% identity
```

NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]

```
298393
Seq. No.
                  LIB3151-007-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  177
                  4.0e-13
E value
Match length
                  71
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  298394
Seq. No.
                  LIB3151-007-Q1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22516
BLAST score
                  160
E value
                  8.0e-85
Match length
                  312
                  88
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                  298395
                  LIB3151-007-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  230
E value
                  2.0e-27
Match length
                  119
% identity
                   60
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   298396
Seq. No.
Seq. ID
                  LIB3151-007-Q1-K1-C5
                  BLASTX
Method
                   g419803
NCBI GI
BLAST score
                   162
                   6.0e-16
E value
Match length
                   109
% identity
                   46
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                   298397
Seq. No.
                  LIB3151-007-Q1-K1-D11
Seq. ID
                  BLASTN
Method
NCBI GI
                   g22514
BLAST score
                   69
E value
                   6.0e-31
Match length
                   125
                   89
% identity
                  Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
NCBI Description
```

```
Seq. No.
                   298398
                   LIB3151-007-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141616
BLAST score
                   290
E value
                   4.0e-26
Match length
                   118
% identity
                   52
                   ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                   >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.
                   298399
Seq. ID
                   LIB3151-007-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q141605
BLAST score
                   186
E value
                   3.0e-14
Match length
                   62
                   68
% identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   298400
Seq. ID
                   LIB3151-007-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   q2832243
BLAST score
                   358
E value
                   5.0e-34
Match length
                   126
% identity
                   61
NCBI Description
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   298401
Seq. No.
Seq. ID
                   LIB3151-007-Q1-K1-F9
Method
                   BLASTN
NCBI GI
                   q22516
                   133
BLAST score
E value
                   1.0e-68
                   241
Match length
% identity
                   89
                   Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
NCBI Description
Seq. No.
                   298402
Seq. ID
                   LIB3151-007-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g141617
                   353
BLAST score
E value
                   2.0e-33
                   82
Match length
                   80
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
```

>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

```
Seq. No.
                  298403
                  LIB3151-007-Q1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168673
BLAST score
                   46
E value
                  7.0e-17
Match length
                   66
                   92
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
Seq. No.
                  298404
Seq. ID
                  LIB3151-007-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                   q141597
BLAST score
                   313
                   1.0e-28
E value
Match length
                   140
% identity
                   57
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   298405
                  LIB3151-007-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                   q141597
NCBI GI
BLAST score
                   286
E value
                   9.0e-26
Match length
                   102
% identity
                   66
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   298406
Seq. No.
Seq. ID
                   LIB3151-008-Q1-K1-A11
Method
                   BLASTX
                   g82660
NCBI GI
                   156
BLAST score
                   8.0e-11
E value
                   64
Match length
                   55
% identity
                   19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi 809117_emb_CAA24720_ (V01473) zein [Zea mays]
                   298407
Seq. No.
Seq. ID
                   LIB3151-008-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   g168701
                   407
BLAST score
                   9.0e-40
E value
```

(M60837) zein [Zea mays]

120

73

Match length

NCBI Description

% identity

```
298408
Seq. No.
                  LIB3151-008-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  q82660
NCBI GI
BLAST score
                  331
                  6.0e-31
E value
                  94
Match length
                  72
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb_CAA24720_ (V01473) zein [Zea mays]
                  298409
Seq. No.
Seq. ID
                  LIB3151-008-Q1-K1-C10
Method
                  BLASTX
                  g168701
NCBI GI
BLAST score
                  288
                  7.0e-26
E value
                  89
Match length
                  62
% identity
NCBI Description (M60837) zein [Zea mays]
                  298410
Seq. No.
                  LIB3151-008-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141616
BLAST score
                  210
                   6.0e-17
E value
Match length
                  85
                  52
% identity
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                   298411
Seq. No.
                  LIB3151-008-Q1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                   q508545
BLAST score
                   359
                   3.0e - 34
E value
                   123
Match length
% identity
NCBI Description (L34340) zein [Zea mays]
                   298412
Seq. No.
                   LIB3151-008-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629861
BLAST score
                   394
E value
                   3.0e-38
Match length
                   138
                   61
% identity
                   zein Zd1, 19K - maize >gi_535020_emb CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
```

Seq. ID LIB3151-008-Q1-K1-F12

Method BLASTN NCBI GI g22514

```
BLAST score
E value
                    3.0e-43
Match length
                    226
                    85
% identity
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)
                    298414
Seq. No.
                    LIB3151-008-Q1-K1-G12
Seq. ID
Method
                    BLASTX
                    g141617
NCBI GI
BLAST score
                    293
                    2.0e-26
E value
Match length
                    98
% identity
                    57
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                    >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    298415
Seq. No.
                    LIB3151-009-Q1-K1-A8
Seq. ID
                    BLASTX
Method
NCBI GI
                    g141605
BLAST score
                    201
E value
                    8.0e-16
                    84
Match length
                    55
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                    >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                    \overline{\text{maize}} > \overline{\text{gi}} = 168\overline{68}0 \text{ (M12145)}  19 kDa zein protein [Zea mays]
                    298416
Seq. No.
Seq. ID
                    LIB3151-009-Q1-K1-C10
                    BLASTN
Method
NCBI GI
                    q168665
BLAST score
                    41
                    4.0e-14
E value
                    153
Match length
% identity
                    82
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                    298417
Seq. No.
                    LIB3151-009-Q1-K1-C6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g168695
BLAST score
                    249
E value
                    1.0e-21
                    79
Match length
                    62
% identity
                     (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                    zein gamma [Zea mays]
                    298418
Seq. No.
                    LIB3151-009-Q1-K1-C8
Seq. ID
```

BLASTN

g168704

Method NCBI GI

NCBI Description



```
BLAST score
                  1.0e-09
E value
                  42
Match length
                  95
% identity
NCBI Description Zea mays zein protein gene, complete cds
                  298419
Seq. No.
Seq. ID
                  LIB3151-009-Q1-K1-C9
Method
                  BLASTN
                  g22544
NCBI GI
                  124
BLAST score
                  3.0e-63
E value
                  144
Match length
                  97
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  298420
Seq. No.
                  LIB3151-009-Q1-K1-D2
Seq. ID
                  BLASTN
Method
                  g508544
NCBI GI
BLAST score
                  118
                  9.0e-60
E value
                  238
Match length
                  88
% identity
                  Zea mays 24-kD alpha-zein gene (floury2), complete cds
NCBI Description
Seq. No.
                  298421
Seq. ID
                  LIB3151-009-Q1-K1-D8
                  BLASTX
Method
                  g2832243
NCBI GI
BLAST score
                   336
E value
                  1.0e-31
Match length
                  100
                   72
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
Seq. No.
                   298422
Seq. ID
                  LIB3151-009-Q1-K1-E2
                   BLASTX
Method
                   q3122673
NCBI GI
BLAST score
                   236
                   4.0e-20
E value
Match length
                   62
                   74
% identity
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb_CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   298423
Seq. No.
                   LIB3151-009-Q1-K1-E6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g168704
BLAST score
                   45
                   2.0e-16
E value
Match length
                   117
% identity
                   85
```

Zea mays zein protein gene, complete cds

seg. No.

Seq. ID

298429

LIB3151-010-Q1-K1-B5



```
298424
Seq. No.
Seq. ID
                  LIB3151-009-Q1-K1-G10
                  BLASTX
Method
NCBI GI
                  g141612
BLAST score
                  251
                  5.0e-30
E value
                  108
Match length
                  36
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
NCBI Description
                  >gi 72306 pir ZIZMC2 22K zein precursor (clone cZ22C2) -
                  maize (fragment) >gi 168688 (M12141) 22 kDa zein protein
                  [Zea mays]
                  298425
Seq. No.
Seq. ID
                  LIB3151-009-Q1-K1-G6
                  BLASTN
Method
NCBI GI
                  g1037129
BLAST score
                  241
                  1.0e-133
E value
                  325
Match length
                  94
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298426
Seq. No.
Seq. ID
                  LIB3151-009-Q1-K1-H2
                  BLASTX
Method
                  g224508
NCBI GI
BLAST score
                  386
                  6.0e-39
E value
Match length
                  119
                  75
% identity
NCBI Description zein A20 [Zea mays]
                  298427
Seq. No.
Seq. ID
                  LIB3151-009-Q1-K1-H9
Method
                  BLASTN
NCBI GI
                  g22516
                  50
BLAST score
E value
                  2.0e-19
Match length
                  82
                  90
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                  298428
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-B10
Method
                  BLASTX
                  g419803
NCBI GI
BLAST score
                  380
                  1.0e-36
E value
Match length
                   112
% identity
                   66
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
```

```
BLASTN
Method
NCBI GI
                  q168685
BLAST score
                   60
                  3.0e-25
E value
Match length
                  248
% identity
                  82
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
                  298430
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-C8
Method
                  BLASTN
NCBI GI
                  g22288
BLAST score
                  54
                  1.0e-21
E value
Match length
                  174
% identity
                  83
NCBI Description Maize mRNA fragment for endosperm glutelin-2
                  298431
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g168697
BLAST score
                   301
E value
                   2.0e-27
Match length
                   86
% identity
                  77
NCBI Description (M60835) zein [Zea mays]
                   298432
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                   g168695
BLAST score
                   224
E value
                   2.0e-18
Match length
                   106
                   50
% identity
                   (M16218) gamma zein [Zea mays] >gi 225315 prf 1211356A
NCBI Description
                   zein gamma [Zea mays]
                   298433
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-D7
Method
                  BLASTN
```

Method BLASTN
NCBI GI g22445
BLAST score 38
E value 4.0e-12
Match length 98
% identity 85

NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 298434

Seq. ID LIB3151-010-Q1-K1-E9

Method BLASTN
NCBI GI g22172
BLAST score 72
E value 2.0e-32
Match length 124
% identity 90



```
NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit
                  298435
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-F2
                  BLASTN
Method
                  g168665
NCBI GI
BLAST score
                  208
E value
                  1.0e-113
Match length
                  236
% identity
                  97
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                  298436
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g419803
BLAST score
                  285
                  1.0e-25
E value
Match length
                  110
% identity
                  53
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
NCBI Description
                  298437
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-G1
Method
                  BLASTX
                  g100938
NCBI GI
BLAST score
                  200
                  8.0e-16
E value
Match length
                  84
                  56
% identity
                  zein precursor - maize >gi 22442 emb CAA32513 (X14335)
NCBI Description
                  zein precursor (AA -21 to 90) [Zea mays]
                  298438
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  182
                  2.0e-13
E value
Match length
                  101
                  46
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  298439
Seq. No.
Seq. ID
                  LIB3151-010-Q1-K1-H7
Method
                  BLASTN
NCBI GI
                  q22516
BLAST score
                  287
E value
                  1.0e-160
Match length
                  329
% identity
                  97
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
```

Seq. ID LIB3151-011-Q1-K1-A11

Method BLASTN



```
g168665
NCBI GI
                  163
BLAST score
                  1.0e-86
E value
                  230
Match length
                  94
% identity
                  Maize 16-kDa zein-2 mRNA, complete cds
NCBI Description
                  298441
Seq. No.
                  LIB3151-011-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121472
BLAST score
                  158
                  3.0e-11
E value
Match length
                  41
                  73
% identity
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                  (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                  [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                  mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
Seq. No.
                  298442
                  LIB3151-011-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                  g224508
NCBI GI
                  270
BLAST score
                  6.0e-24
E value
                  79
Match length
                  78
% identity
NCBI Description zein A20 [Zea mays]
Seq. No.
                  298443
                  LIB3151-011-Q1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g168691
BLAST score
                  189
                  1.0e-14
E value
                  73
Match length
                  55
% identity
NCBI Description (M29628) zein [Zea mays]
                  298444
Seq. No.
Seq. ID
                  LIB3151-011-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q419803
BLAST score
                  264
                  3.0e-23
E value
                   92
Match length
                   59
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
```

Seq. ID LIB3151-011-Q1-K1-C8

Method BLASTN NCBI GI g1037129

% identity

82 NCBI Description (M60837) zein [Zea mays]



```
BLAST score
                  1.0e-129
E value
                  362
Match length
                  91
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298446
Seq. No.
                  LIB3151-011-Q1-K1-E11
Seq. ID
Method
                  BLASTN
                  g22549
NCBI GI
BLAST score
                  52
                  1.0e-20
E value
Match length
                  148
% identity
                  84
NCBI Description Maize gene for a 27kDa storage protein, zein
                  298447
Seq. No.
                  LIB3151-011-Q1-K1-E6
Seq. ID
Method
                  BLASTN
                  g22544
NCBI GI
BLAST score
                  109
E value
                   2.0e-54
                  133
Match length
% identity
                   96
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                   298448
Seq. No.
                  LIB3151-011-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                   g629861
NCBI GI
                   236
BLAST score
                   9.0e-28
E value
                   98
Match length
                   66
% identity
                  zein Zd1, 19K - maize >gi 535020_emb CAA47639_ (X67203)
NCBI Description
                   zein Zdl (19 kDa zein) [Zea mays]
                   298449
Seq. No.
Seq. ID
                   LIB3151-011-Q1-K1-F3
                   BLASTX
Method
NCBI GI
                   g2832243
BLAST score
                   141
                   2.0e-15
E value
Match length
                   102
                   56
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   298450
Seq. No.
Seq. ID
                   LIB3151-011-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   q168701
BLAST score
                   548
                   3.0e-56
E value
Match length
                   138
```

```
298451
Seq. No.
                  LIB3151-011-Q1-K1-H11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g168698
BLAST score
                  46
                  7.0e-17
E value
                  157
Match length
% identity
                  83
NCBI Description Z.mays zein mRNA, complete cds
Seq. No.
                  298452
                  LIB3151-012-Q1-K1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g535019
BLAST score
                  64
E value
                  2.0e-27
Match length
                  136
                  44
% identity
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
                  298453
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  q141610
BLAST score
                  172
                  3.0e-12
E value
Match length
                  64
% identity
                  56
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                  298454
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-A8
                  BLASTX
Method
                  q419803
NCBI GI
                  247
BLAST score
                  3.0e-21
E value
Match length
                  84
                   58
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                   298455
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-B7
                  BLASTX
Method
                  g82660
NCBI GI
BLAST score
                   450
                   9.0e-45
E value
                  147
Match length
                   65
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
                   298456
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-C10
```

BLASTN

q168704

Method NCBI GI

```
68
BLAST score
                    3.0e-30
E value
                    87
Match length
                    94
% identity
                   Zea mays zein protein gene, complete cds
NCBI Description
                    298457
Seq. No.
                    LIB3151-012-Q1-K1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q141604
BLAST score
                    415
E value
                    1.0e-40
Match length
                    132
% identity
                    71
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
NCBI Description
                    >qi 72310 pir ZIZM91 19K zein precursor (clone cZ19C1) -
                    \overline{\text{maize}} > \overline{\text{gi}} = 168\overline{678} (M12146) 19 kDa zein protein [Zea mays]
Seq. No.
                    298458
                    LIB3151-012-Q1-K1-C6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g224507
BLAST score
                    173
                    1.0e-19
E value
                    93
Match length
% identity
                    61
                                                                            17
NCBI Description
                   zein Al [Zea mays]
                    298459
Seq. No.
                    LIB3151-012-Q1-K1-D12
Seq. ID
Method
                    BLASTN
NCBI GI
                    g168677
BLAST score
                    34
                    6.0e-10
E value
Match length
                    50
                    94
% identity
                    Maize 19 kDa zein mRNA, clone cZ19C1, complete cds
NCBI Description
                    298460
Seq. No.
Seq. ID
                    LIB3151-012-Q1-K1-D3
                    BLASTX
Method
NCBI GI
                    g141617
                    229
BLAST score
                    5.0e-19
E value
Match length
                    100
                    51
% identity
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                    >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
```

Seq. ID LIB3151-012-Q1-K1-D6

Method BLASTN
NCBI GI g168484
BLAST score 192

Seq. ID



```
1.0e-104
E value
                  386
Match length
                  94
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                  298462
Seq. No.
                  LIB3151-012-Q1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g224507
                  178
BLAST score
                  4.0e-13
E value
Match length
                  63
                  60
% identity
NCBI Description zein A1 [Zea mays]
                  298463
Seq. No.
                  LIB3151-012-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g100940
NCBI GI
BLAST score
                  265
                  3.0e-23
E value
Match length
                  91
% identity
                  60
NCBI Description zein zA1 - maize
                  298464
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-E6
Method
                  BLASTN
                  g168675
NCBI GI
                  70
BLAST score
                  2.0e-31
E value
                  114
Match length
% identity
                  91
NCBI Description Maize mutant zein (zE19) gene, complete cds
                  298465
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-F11
Method
                  BLASTN
                  g22516
NCBI GI
BLAST score
                   363
                  0.0e + 00
E value
Match length
                   423
                  96
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                  298466
Seq. No.
                  LIB3151-012-Q1-K1-F5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g168692
BLAST score
                   62
E value
                  2.0e-26
Match length
                  216
                  88
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG7
Seq. No.
                   298467
```

41919

LIB3151-012-Q1-K1-G5

```
BLASTX
Method
                  g1332579
NCBI GI
BLAST score
                  642
                  2.0e-67
E value
                  151
Match length
% identity
NCBI Description
                  (X98063) polyubiquitin [Pinus sylvestris]
                  298468
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-G7
Method
                  BLASTX
                  g168695
NCBI GI
BLAST score
                  143
                  9.0e-09
E value
Match length
                  28
                  93
% identity
                  (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
Seq. No.
                  298469
Seq. ID
                  LIB3151-012-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q121472
BLAST score
                  254
                  9.0e-23
E value
Match length
                  118
                  50
% identity
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                  (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                  [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                  mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
                  298470
Seq. No.
Seq. ID
                  LIB3151-012-Q1-K1-H7
                  BLASTN
Method
                  q22514
NCBI GI
BLAST score
                  89
                  2.0e-42
E value
Match length
                  222
                  90
% identity
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)
Seq. No.
                  298471
Seq. ID
                  LIB3151-012-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  203
                  5.0e-16
E value
Match length
                  59
                  69
% identity
NCBI Description
                  19K zein precursor (clone ZG31A) - maize (fragment)
                  >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
```

Seq. ID LIB3151-013-Q1-K1-B11



Method

BLASTX

```
NCBI GI
                  g951449
                  498
BLAST score
                  2.0e-50
E value
                  149
Match length
                  65
% identity
                  (L46681) aspartic protease precursor [Lycopersicon
NCBI Description
                  esculentum]
                  298473
Seq. No.
                  LIB3151-013-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g2995405
NCBI GI
BLAST score
                  281
E value
                   6.0e-25
                  86
Match length
                   59
% identity
                  (Y12432) polyprotein [Ananas comosus]
NCBI Description
Seq. No.
                   298474
                  LIB3151-013-Q1-K1-B5
Seq. ID
                   BLASTX
Method
                   g3094012
NCBI GI
                   204
BLAST score
                   5.0e-16
E value
                   79
Match length
                   59
% identity
                  (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
NCBI Description
                   298475
Seq. No.
                   LIB3151-013-Q1-K1-B9
Seq. ID
Method
                   BLASTX
                   q3885334
NCBI GI
BLAST score
                   153
                   6.0e-10
E value
Match length
                   73
% identity
                   51
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
                   298476
Seq. No.
                   LIB3151-013-Q1-K1-C2
Seq. ID
Method .
                   BLASTX
NCBI GI
                   g3540180
BLAST score
                   171
E value
                   4.0e-12
Match length
                   84
                   50
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
                   298477
Seq. No.
Seq. ID
                   LIB3151-013-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   g100484
BLAST score
                   512
                   5.0e-52
E value
Match length
                   147
```